

Network Systems
Science & Advanced
Computing
Biocomplexity Institute
& Initiative
University of Virginia

Estimation of COVID-19 Impact in Virginia

February 24th, 2021

(data current to February 22nd – 24th)

Biocomplexity Institute Technical report: TR 2021-022



BIOCOMPLEXITY INSTITUTE

biocomplexity.virginia.edu

About Us

- Biocomplexity Institute at the University of Virginia
 - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
 - Pandemic response for Influenza, Ebola, Zika, and others



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Overview

- **Goal:** Understand impact of COVID-19 mitigations in Virginia
- **Approach:**
 - Calibrate explanatory mechanistic model to observed cases
 - Project based on scenarios for next 4 months
 - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
 - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
 - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

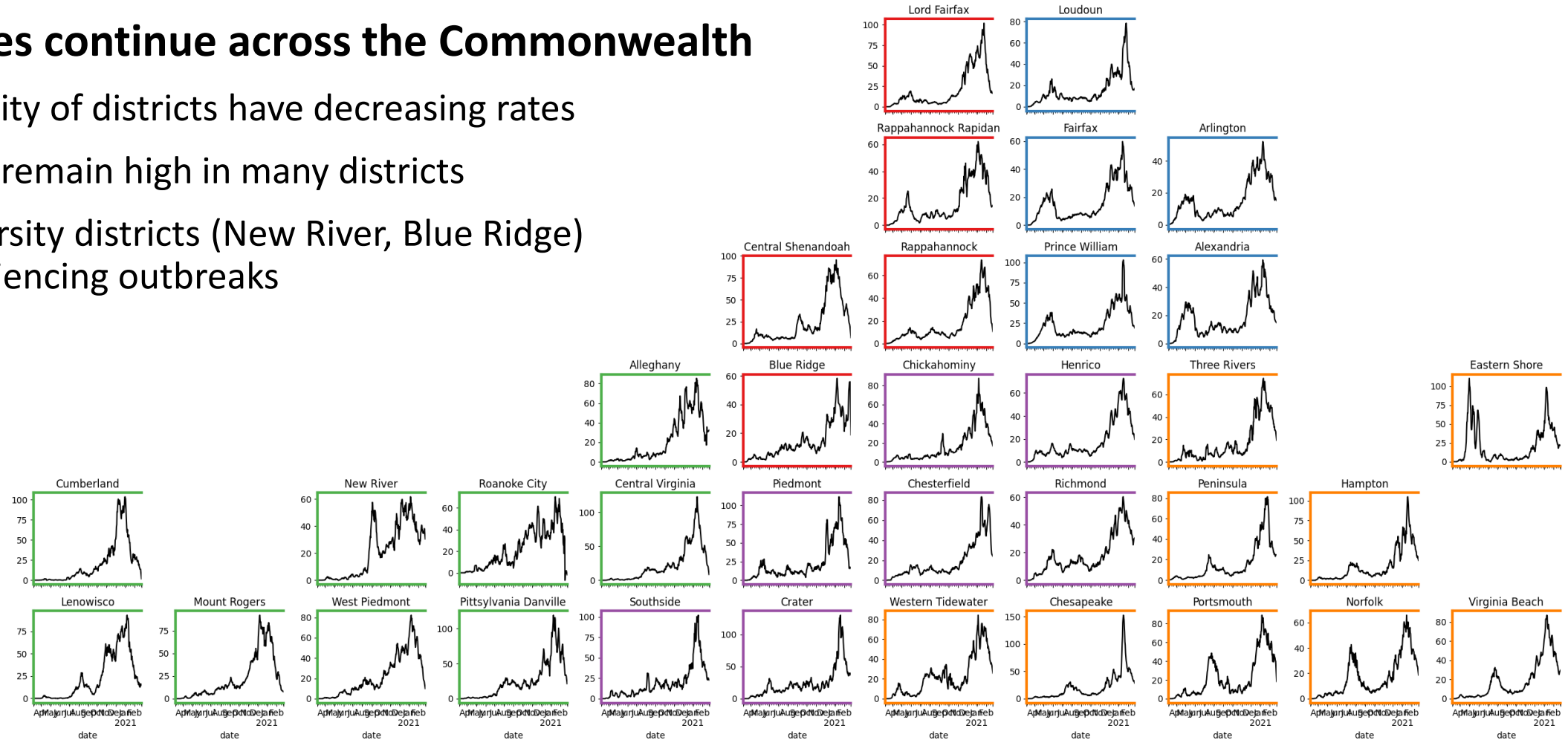
- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 23/100K from 34/100K, US levels decline (to 19 from 23 per 100K)
- Significant progress made in last month, however 92% of VA counties above mean rate of Summer 2020
- Projections are down across Commonwealth, though several districts with universities are notably up
- Recent updates:
 - Variant B.1.1.7 scenarios included and added to control-based scenarios
 - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- The situation is changing rapidly. Models continue to be updated regularly.

Situation Assessment

Case Rate (per 100k) by VDH District

Declines continue across the Commonwealth

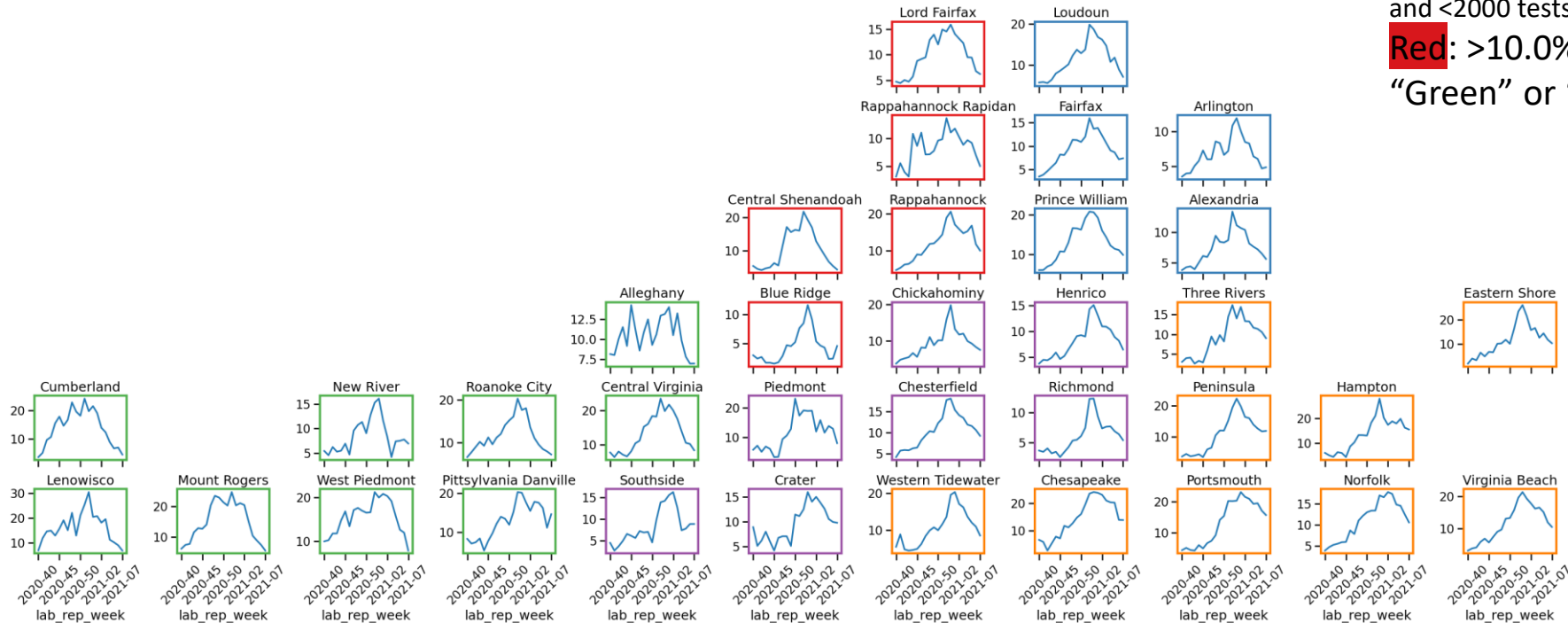
- Majority of districts have decreasing rates
- Rates remain high in many districts
- University districts (New River, Blue Ridge) experiencing outbreaks



Test Positivity by VDH District

Weekly changes in test positivity by district

- Rates continue to decline
- 68 counties classified in the 'Red' category (as of Feb 17th)

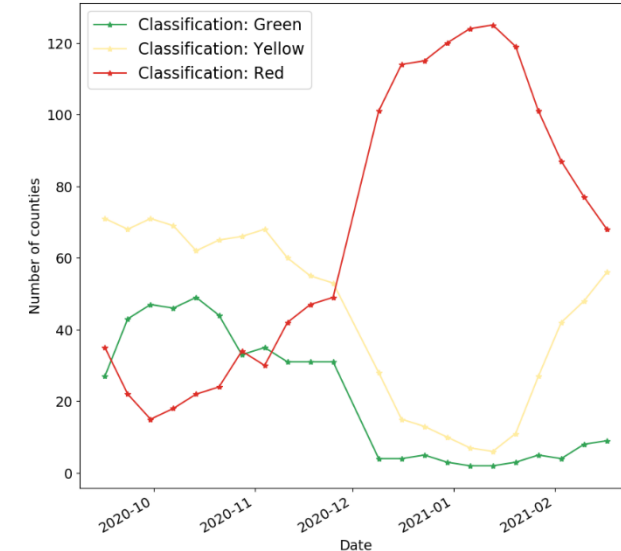


County level test positivity rates for RT-PCR tests.

Green: Test positivity <5.0%
(or with <20 tests in past 14 days)

Yellow: Test positivity 5.0%-10.0% (or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)

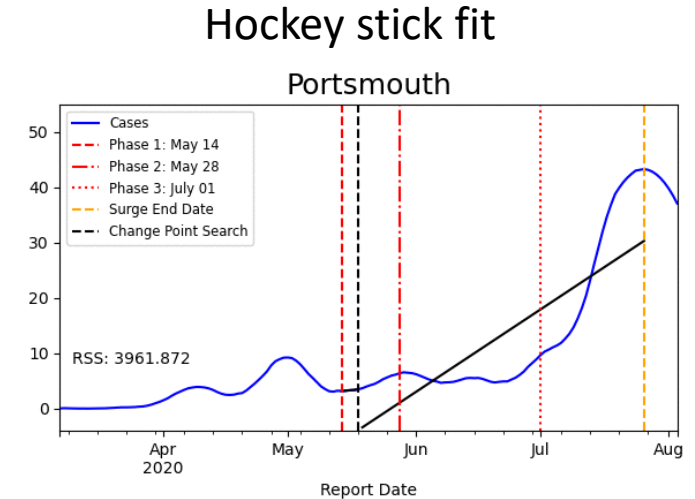
Red: >10.0% and not meeting the criteria for "Green" or "Yellow"



District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory

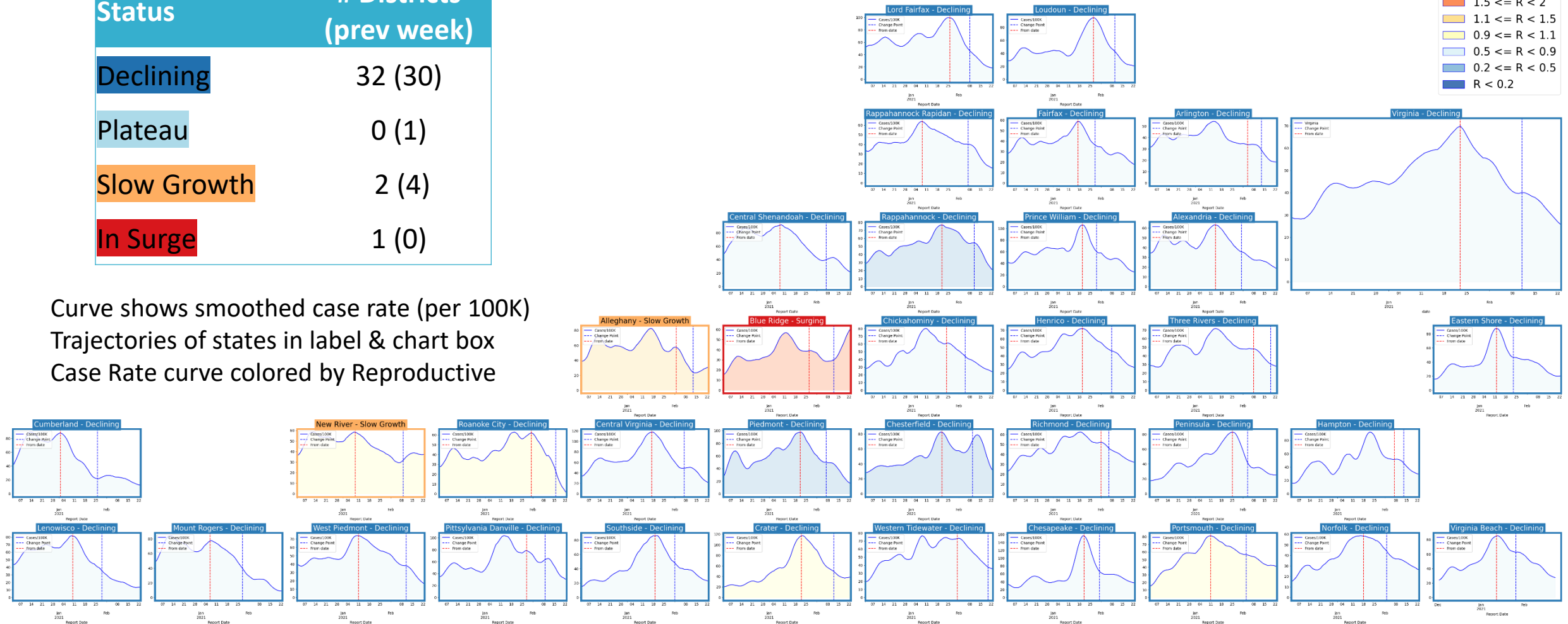


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	33 (30)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	0 (1)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	2 (4)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (0)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	32 (30)
Plateau	0 (1)
Slow Growth	2 (4)
In Surge	1 (0)

Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive



SARS-CoV2 Variants of Concern

Emerging new variants will alter the future trajectory of pandemic and have implications for future control

- Current evidence supports that new variants can:
 - Increase transmissibility
 - Increase severity (more hospitalizations and/or deaths)
 - Limit immunity from prior infection and vaccination

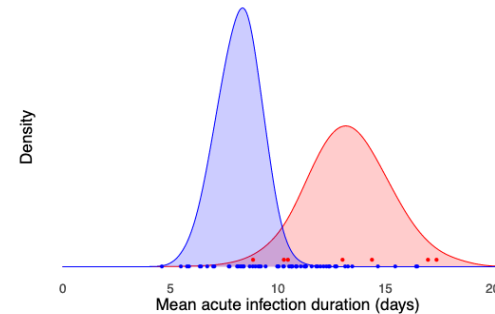
Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia as well as in at least 1,881 cases across 45 states as of Feb 23rd (10-20 day delay for genotyping), will continue to grow rapidly
- [A recent study](#) finds B.1.1.7 to have longer duration which may be the source of increased transmissibility and has implications for isolation durations
- [Estimates based on US growth rates](#) estimate it will predominate (eg reach 50% frequency) by mid to late March and is 35%-45% more transmissible
- [Another study](#) based on sequenced B.1.1.7 now estimates 40-80% more transmissible, though a [study in Lancet](#) also finds B117 infections have no appreciably different clinical course

Lineages Of Concern

LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (SGTF)
B.1.351	B.1.351	20H/501Y.V2	South African variant	October 2020	Nelson Mandela Bay, South African	L241-, L242-, A243-, K417N, E484K, N501Y, D614G	loss of serum antibody neutralization
P.1	B.1.1.28	20J/501Y.V3	Brazilian variant	July 2020	Brazil	K417T, E484K, N501Y, D614G	Increased transmissibility; loss of serum antibody neutralization
CAL.20C	B.1.429			July 2020	Southern California, USA	W152C, L452R, D614G	loss of monoclonal antibody binding
B.1.375	B.1.375			September 2020	Massachusetts, USA	H69-, V70-, D614G	S gene target failure (SGTF)

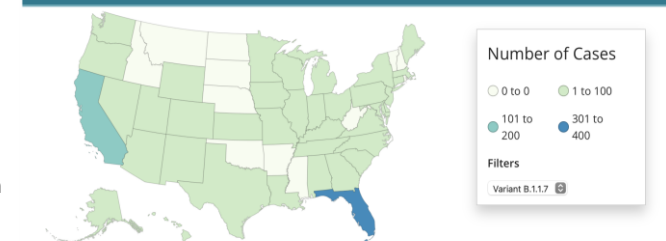
[NIH-NIAID Bacterial-Viral Bioinformatics Resource Center](#)



Variant B.1.1.7 may cause longer infections with similar peak viral concentration compared to non-B.1.1.7 May contribute to B.1.1.7 S increased transmissibility.

<https://dash.harvard.edu/handle/1/37366884>

Variant	Reported Cases in US	Number of States Reporting
B.1.1.7	1,881	45
B.1.351	46	14
P.1	5	4



[CDC Variant Tracking](#)

New variants of SARS-CoV2

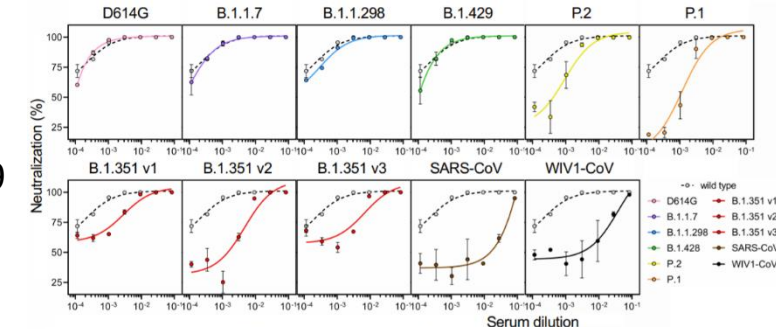
Lineage B.1.351

- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 46 reported cases in 14 states (including Virginia, 21 in South Carolina) as of Feb 23rd
- [New study in Cell](#) demonstrates immune escape across a bank of sera from different COVID-19 patients and vaccine recipients (Pfizer and AstraZeneca)
- [New Experiments](#) show SARS-CoV-2 variants B.1.351 and B.1.1.248 escape from therapeutic antibodies and antibodies induced by infection and vaccination, though [an additional study demonstrated](#) that a single boosting dose of mRNA vaccine restores response

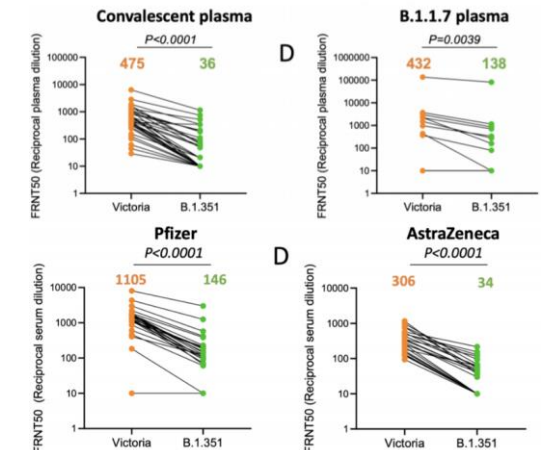
Additional Variants

- Lineage P.1 (similar mutations as in B.1.1.7 and B.1.351):** [First case reported in Minnesota](#) on Jan 25th, now 5 cases in 4 states has caused a [resurgence of hospitalizations in Manaus, Brazil](#) continues this despite estimated [3/4 of the population infected](#)
- Lineage B.1.429 (similar mutations as in B.1.1.7 and B.1.351):** Initially found in Southern California, coincided with surge in Nov and Dec, [found in over half of sequenced samples in LA](#)
- New naming conventions in the works. May cluster these with bird names: Robin 1, Robin 2, Pelican, Yellowhammer, Mockingbird, Bluebird, Quail, etc.

Key Mutations for immunity escape



5 strains harboring receptor-binding domain mutations, including K417N/T, E484K, and N501Y, were highly resistant to neutralization [Medrxiv](#)



Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine induced sera. Neutralization of B.1.351 by sera from naturally infected or 134 vaccinated individuals is significantly reduced, leading in some cases to a complete inability to neutralize B.1.351 virus [Cell](#)

Estimating Daily Reproductive Number

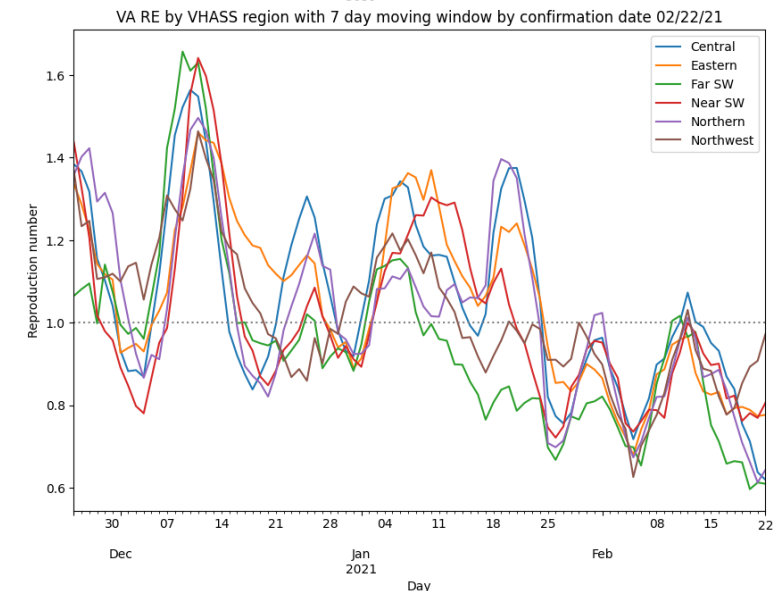
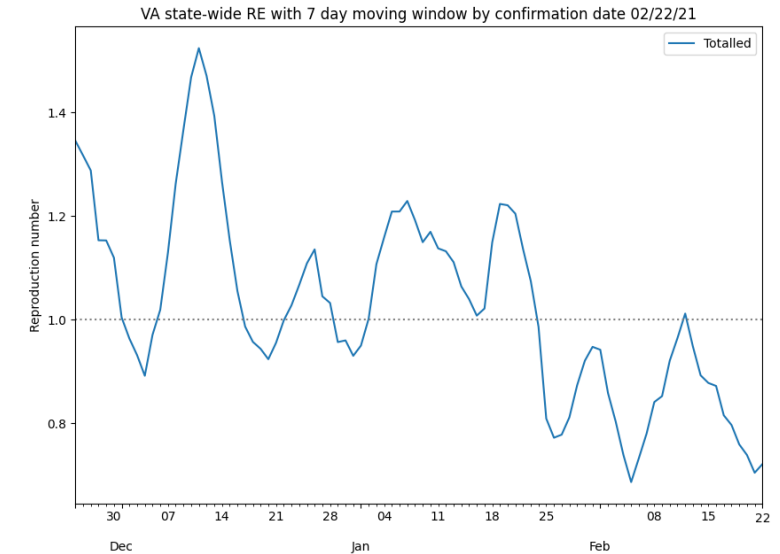
Feb 22nd Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.721	-0.157
Central	0.619	-0.332
Eastern	0.777	-0.049
Far SW	0.610	-0.142
Near SW	0.806	-0.092
Northern	0.643	-0.232
Northwest	0.972	0.089

Methodology

- Wallinga-Teunis method (EpiEstim¹) for cases by **confirmation date**
- Serial interval: 6 days (2 day std dev)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

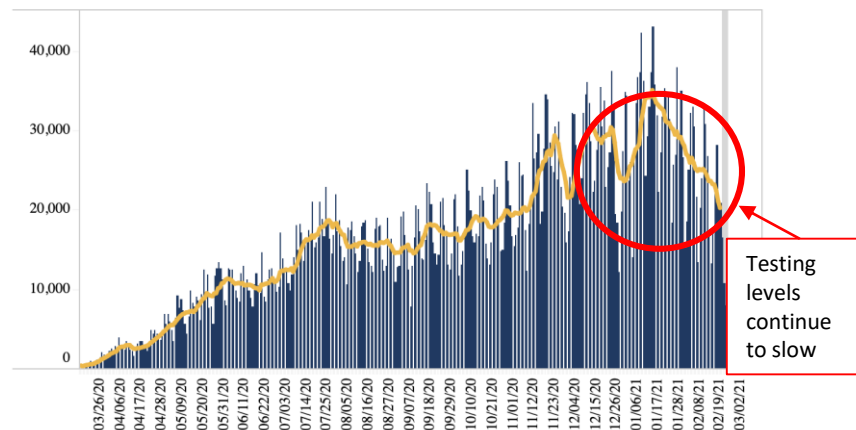
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, <https://doi.org/10.1093/aje/kwt133>



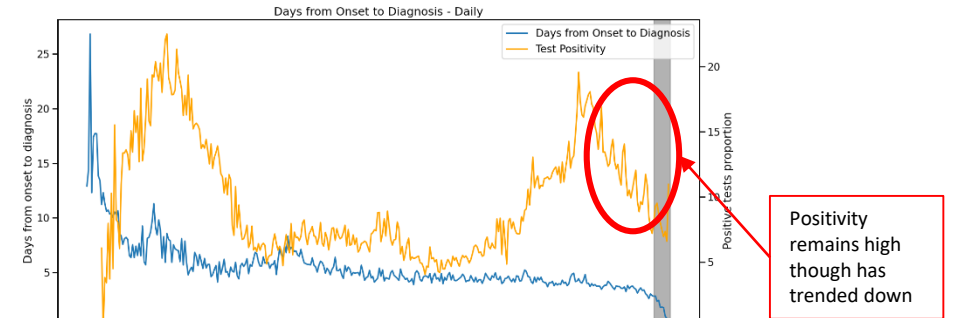
Changes in Case Detection

Timeframe (weeks)	Mean days	% difference from overall mean
May (17-21)	5.7	-18%
June (22-25)	5.8	-17%
July (26-30)	6.1	-12%
Aug (31-34)	4.9	-30%
Sept (35-38)	4.6	-34%
Oct (39-43)	4.5	-36%
Nov (44-47)	4.5	-35%
Dec (48-49)	4.2	-40%
Jan (00-05)	3.8	-46%
Overall (13-05)	6.9	--

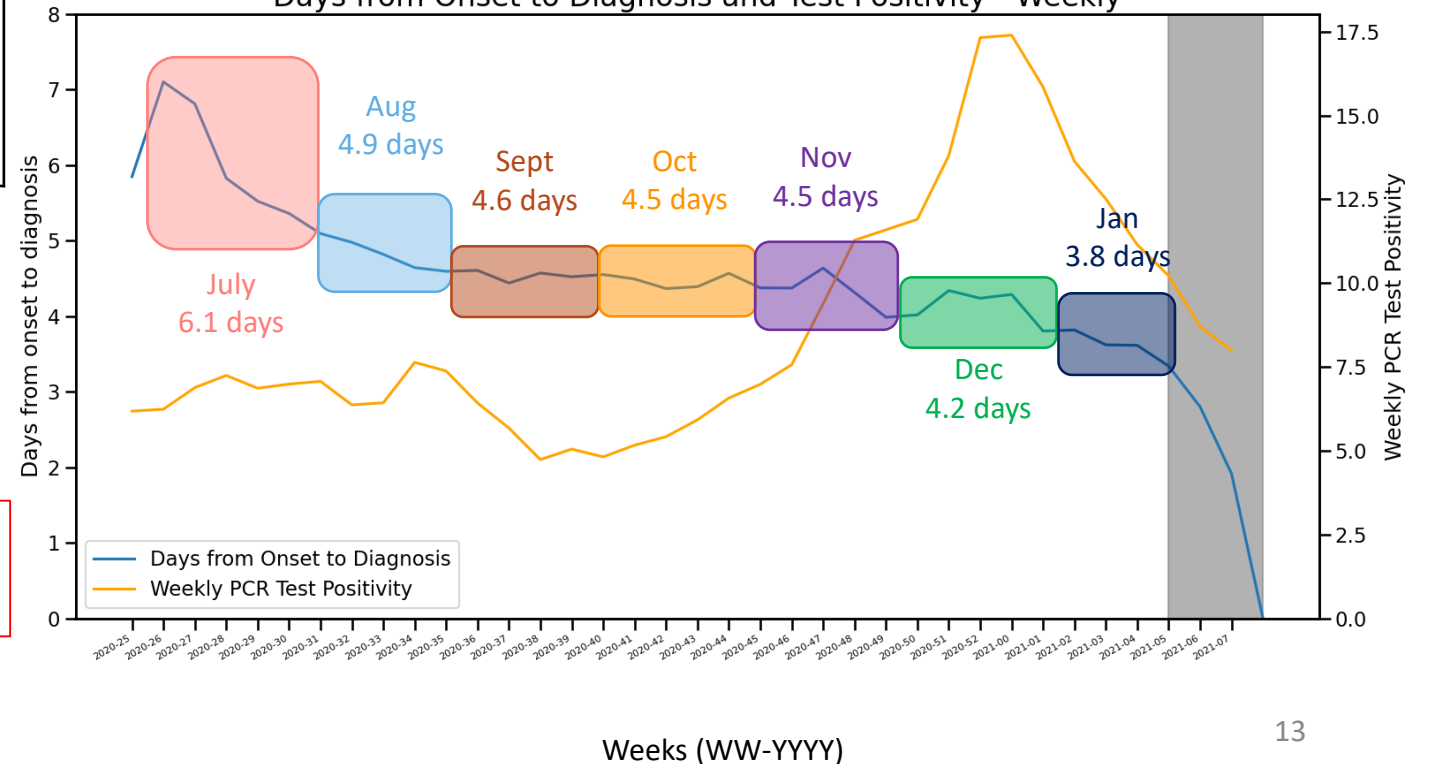
Number of Testing Encounters by Lab Report Date - All Health Districts, PCR Only



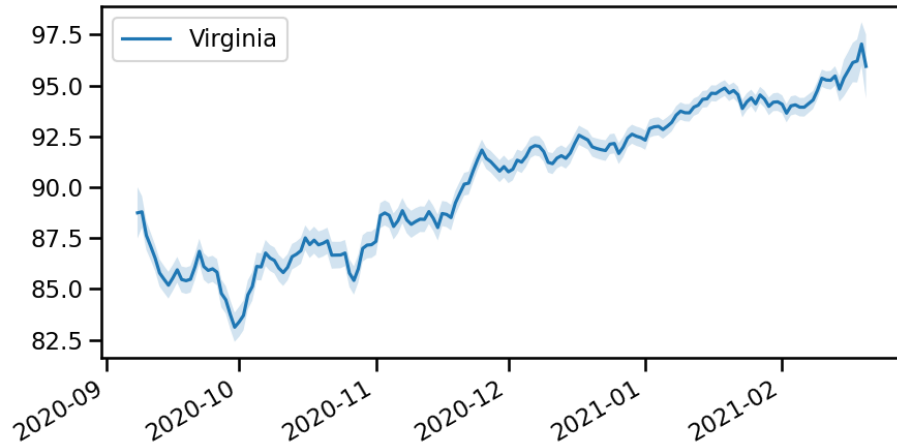
Test positivity vs. Onset to Diagnosis



Days from Onset to Diagnosis and Test Positivity - Weekly



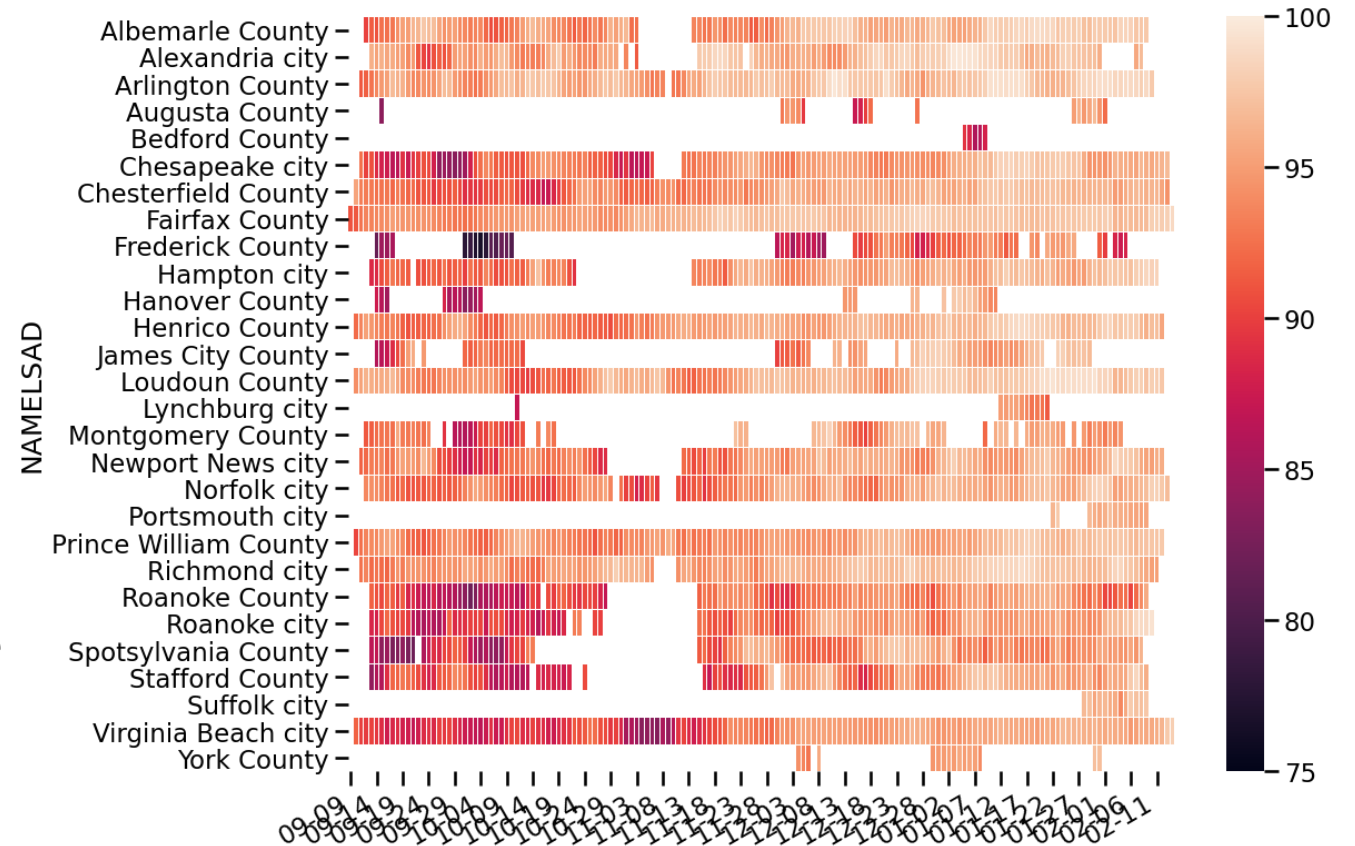
Mask Usage in Virginia



State level mask usage as reported via Facebook surveys has shown steady increase over past three months

- ~88% (early Nov) to ~94% (mid Feb)
- Some variance across the Commonwealth
- ~3000 daily responses from VA

Data Source: <https://covidcast.cmu.edu>

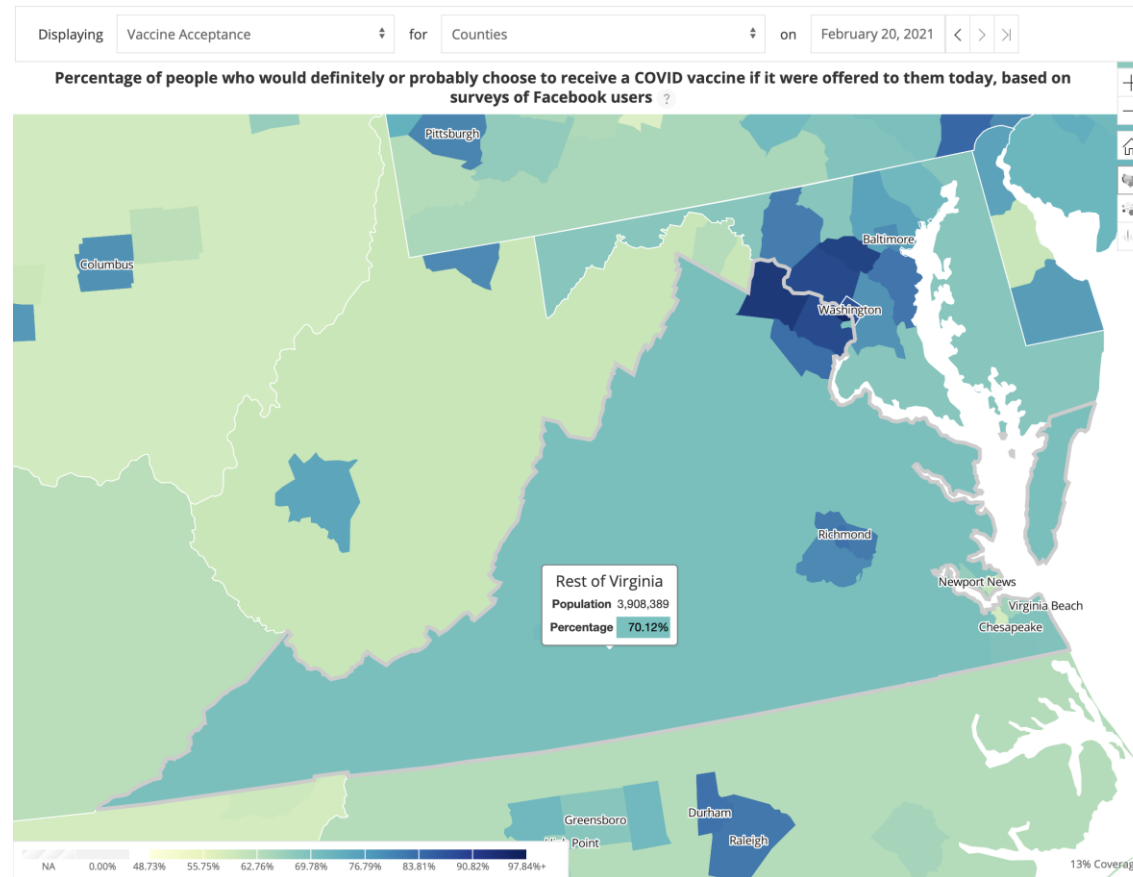


Some county level fluctuations over time, with many counties stabilizing recently.

Vaccine Acceptance

Facebook administered survey:
Percent of people who would definitely or probably choose to receive a COVID vaccine if offered today

VA typically achieves 50-60% coverage with seasonal influenza vaccine (typically over the course of 3 months)



Vaccine Acceptance in Virginia



Acceptance down slightly from January, but has been consistently high:
Nearly $\frac{3}{4}$ of Virginians are likely to choose to be vaccinated if offered today

[COVIDcast Data Explorer](https://covidcast.cmu.edu)

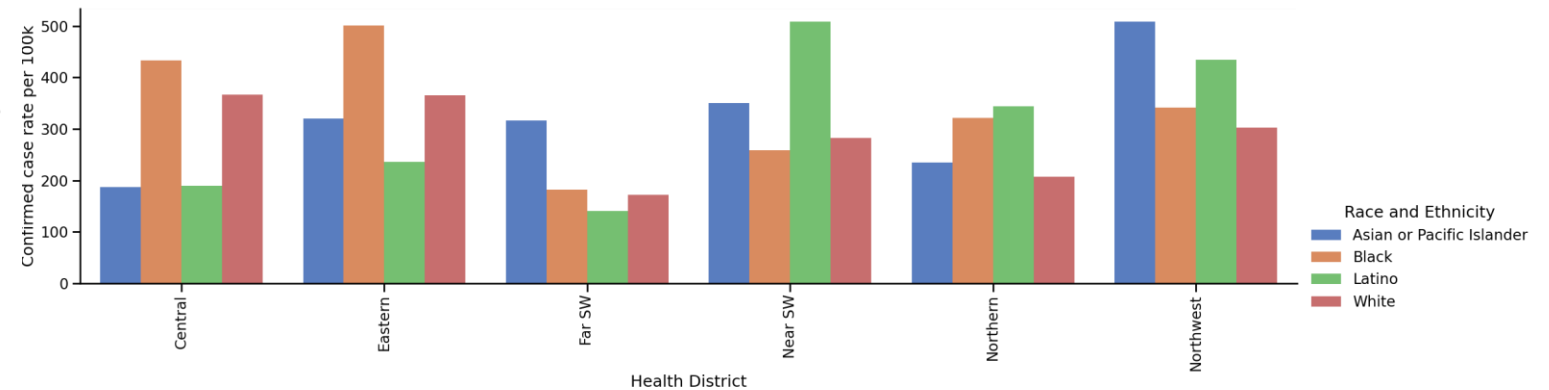
Source: <https://covidcast.cmu.edu>

Race and Ethnicity – Recent Rate Changes (per 100K)

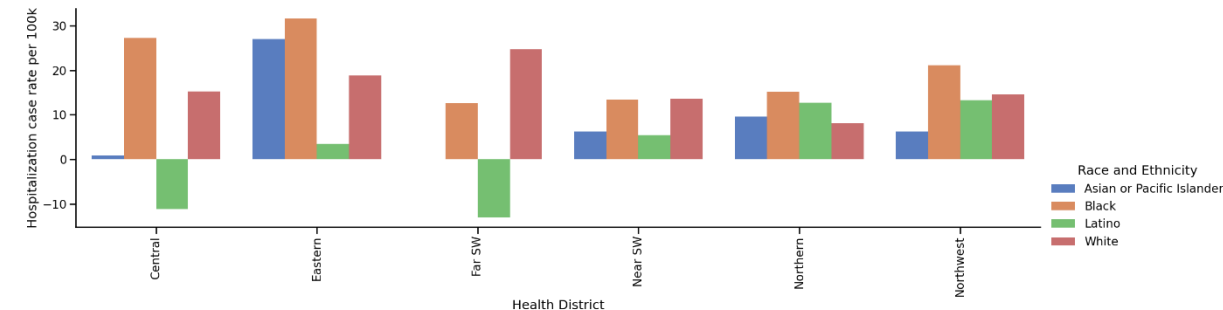
Changes in Race and Ethnicity Rates (per 100k) in past two weeks

- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county

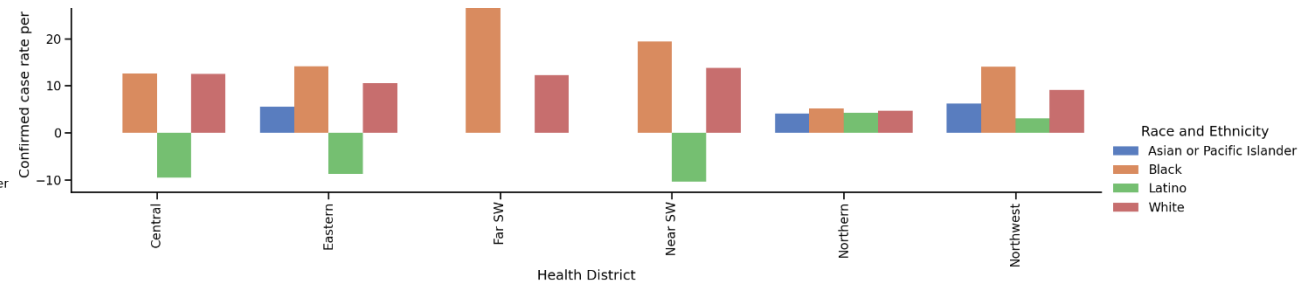
Case Rate



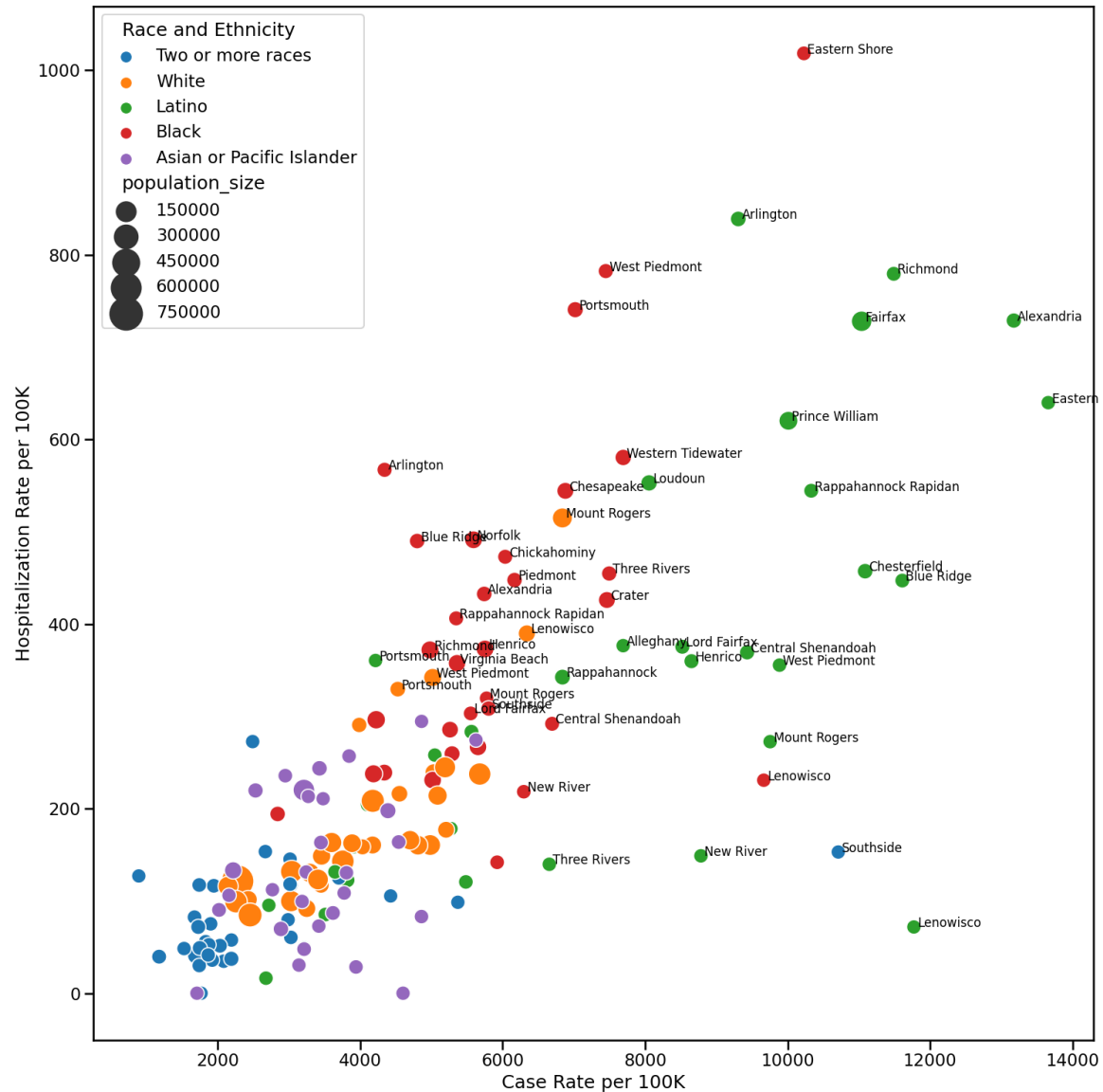
Hospitalization Rate



Death Rate



Race and Ethnicity cases per 100K

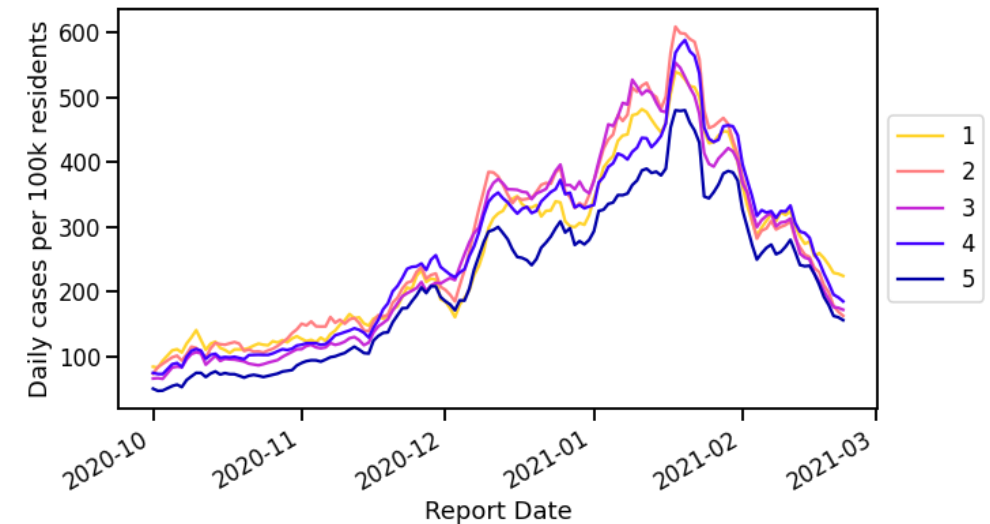


Rates per 100K of each Racial-Ethnic population by Health District

- Each Health District's Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)

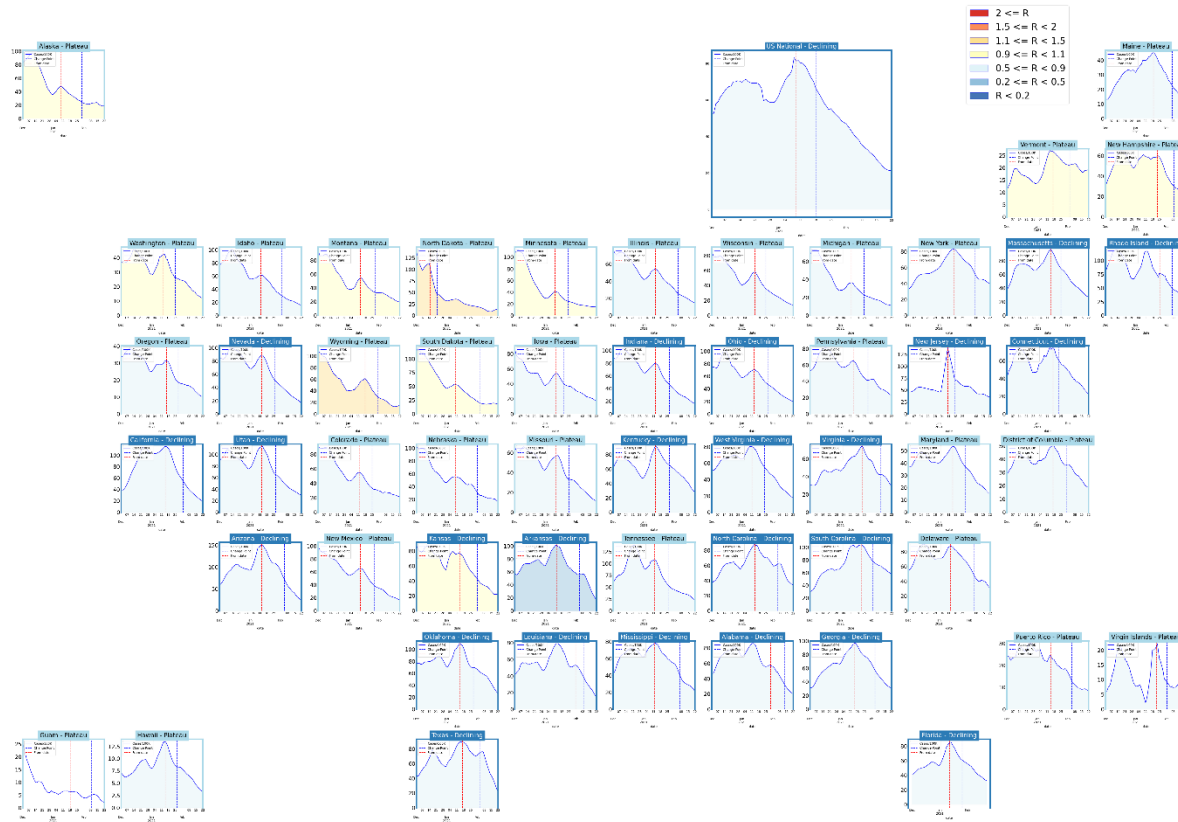
Case rates by zip codes broken into income quintiles

VDH 7-day moving average rate of new COVID-19 cases by zip code average household income (dollars/ household years) quantile



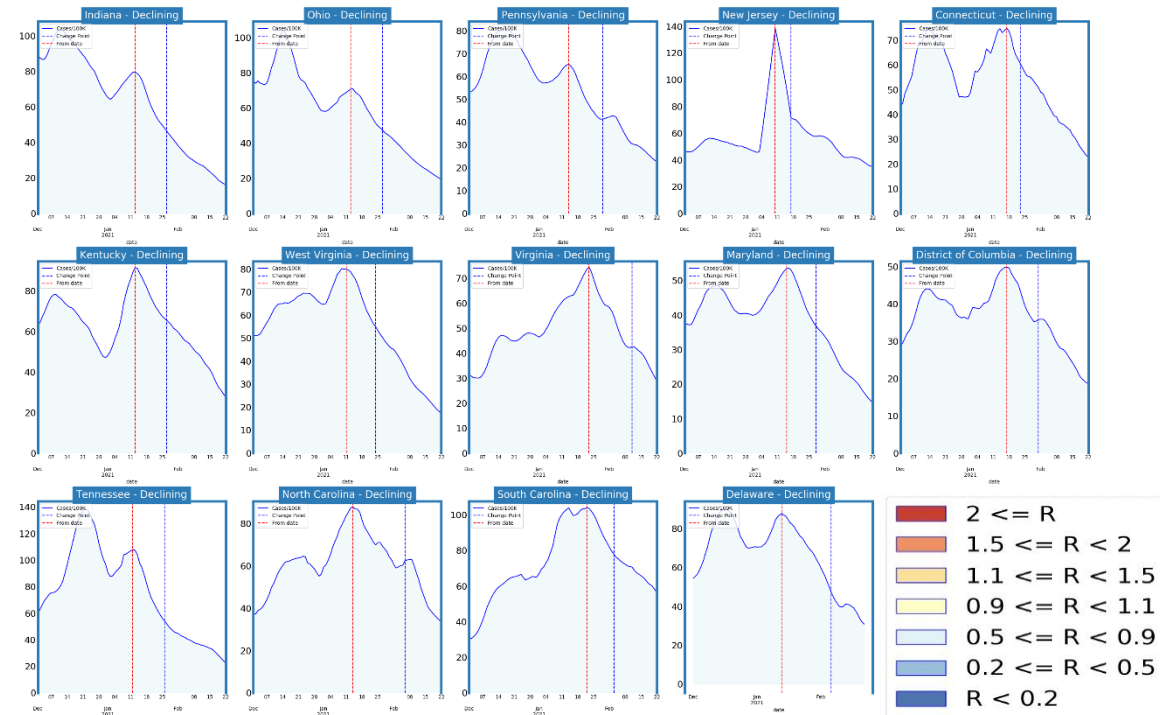
Other State Comparisons

Trajectories of States



- All states are declining (24) or plateaued (30)
- Rates remain elevated, some states declines are leveling off

Virginia and her neighbors

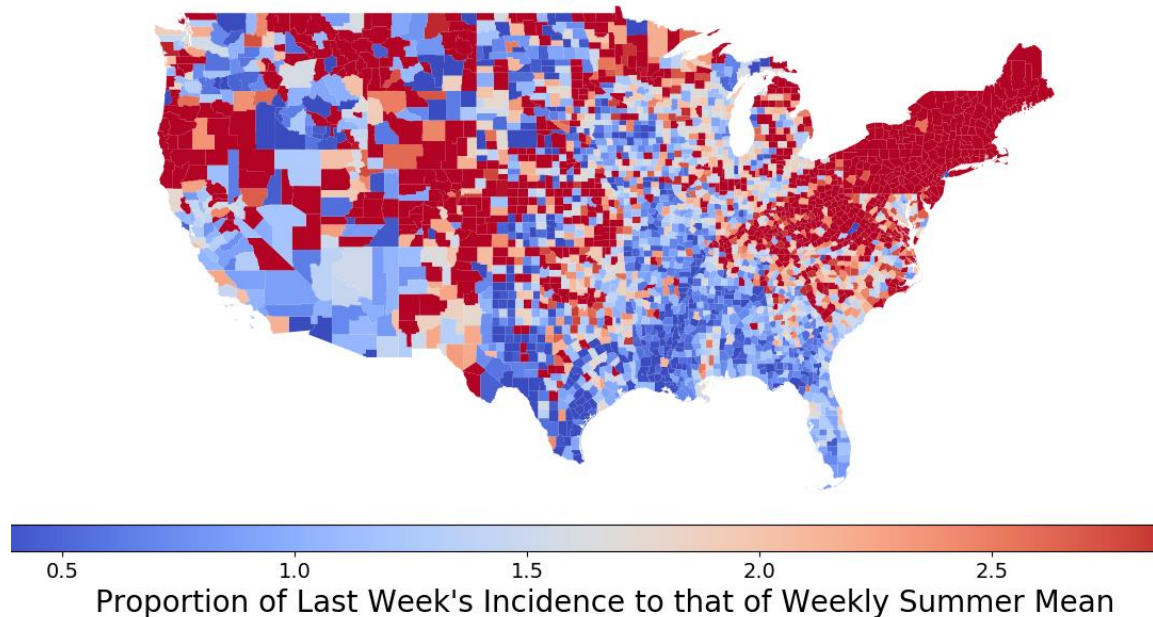


- VA and her neighbors are all declining
- Rates are elevated but retreating to lower levels

Current Week vs. Summer Mean (June-Aug 2020)

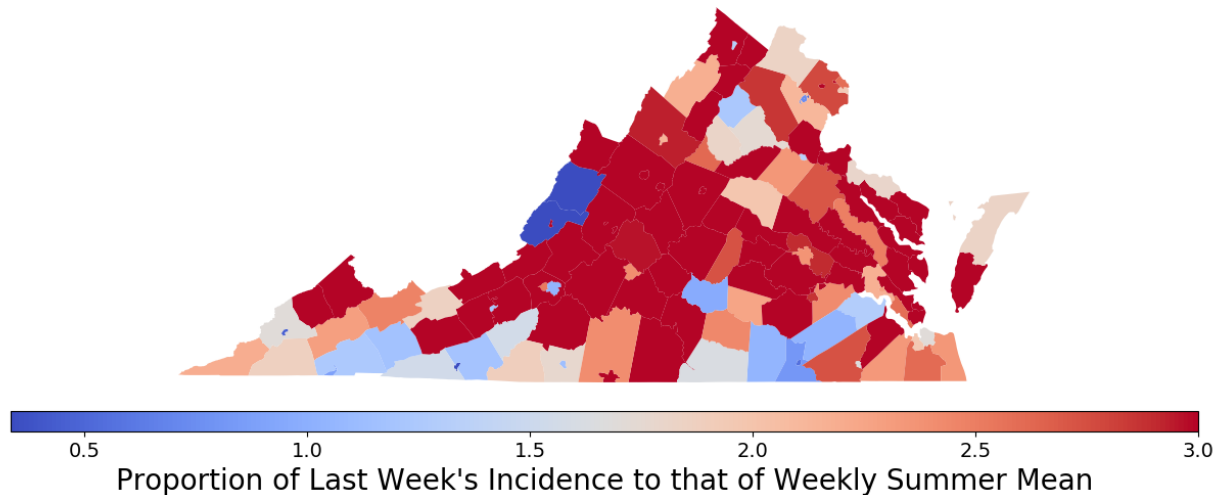
Still some way to go to return to rates experienced during the summer of 2020 (June through August)

Recent Incidence Compared to Weekly Summer Mean by County
Mean: 12.7; Median: 1.78; IQR: 0.95-3.56



- 73% of US counties are above the summer mean case rate
- 93% are now below 50% of their worst weekly case rate

Recent Incidence Compared to Weekly Summer Mean by County
Mean: 3.8; Median: 2.78; IQR: 1.84-4.52



- 92% of VA counties are above the average rate for the summer
- 87% are now below 50% of their worst weekly case rate

Zip code level weekly Case Rate (per 100K)

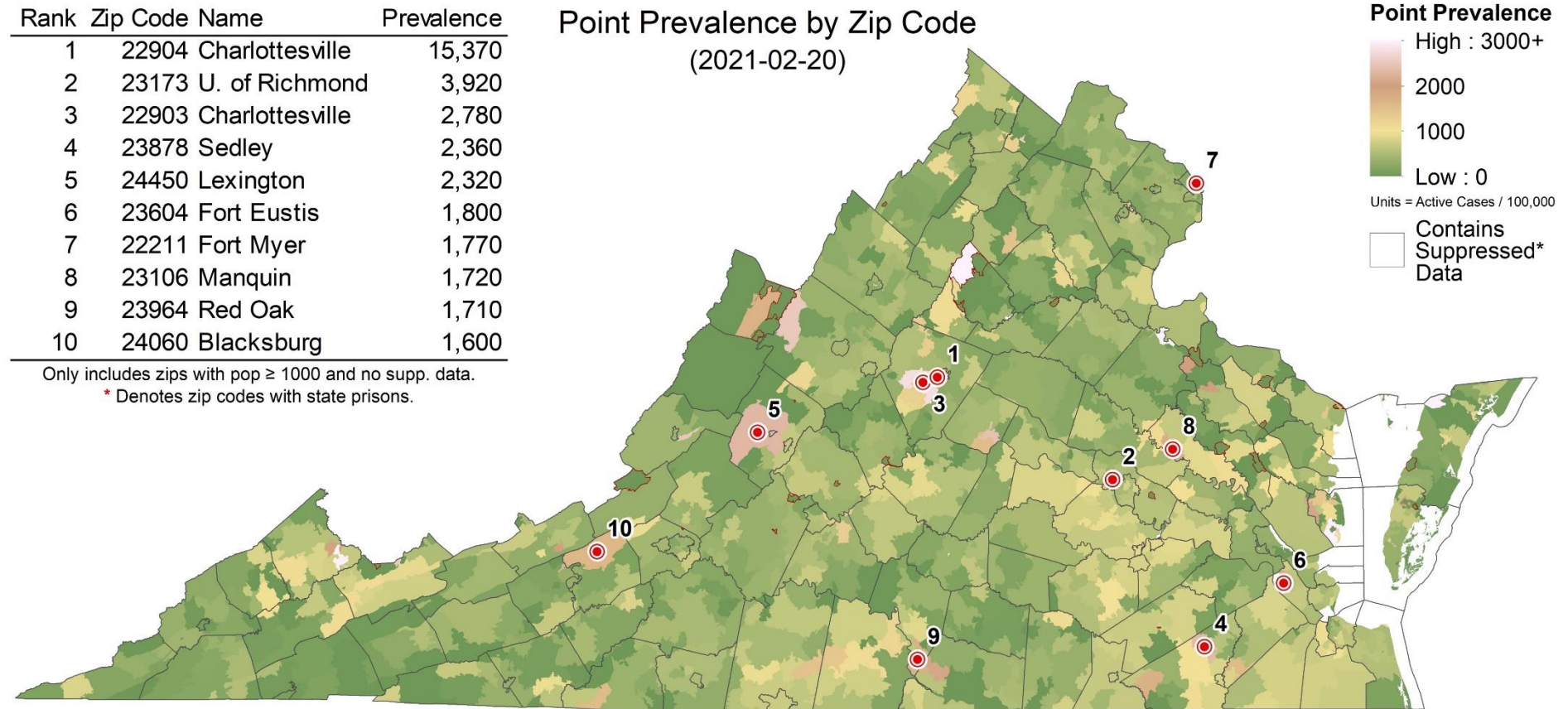
Case Rates in the last week by zip code

- Universities dominate the list
- Concentrations of high rates scattered across the Commonwealth
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prevalence
1	22904	Charlottesville	15,370
2	23173	U. of Richmond	3,920
3	22903	Charlottesville	2,780
4	23878	Sedley	2,360
5	24450	Lexington	2,320
6	23604	Fort Eustis	1,800
7	22211	Fort Myer	1,770
8	23106	Manquin	1,720
9	23964	Red Oak	1,710
10	24060	Blacksburg	1,600

Only includes zips with pop ≥ 1000 and no supp. data.

* Denotes zip codes with state prisons.



Risk of Exposure by Group Size

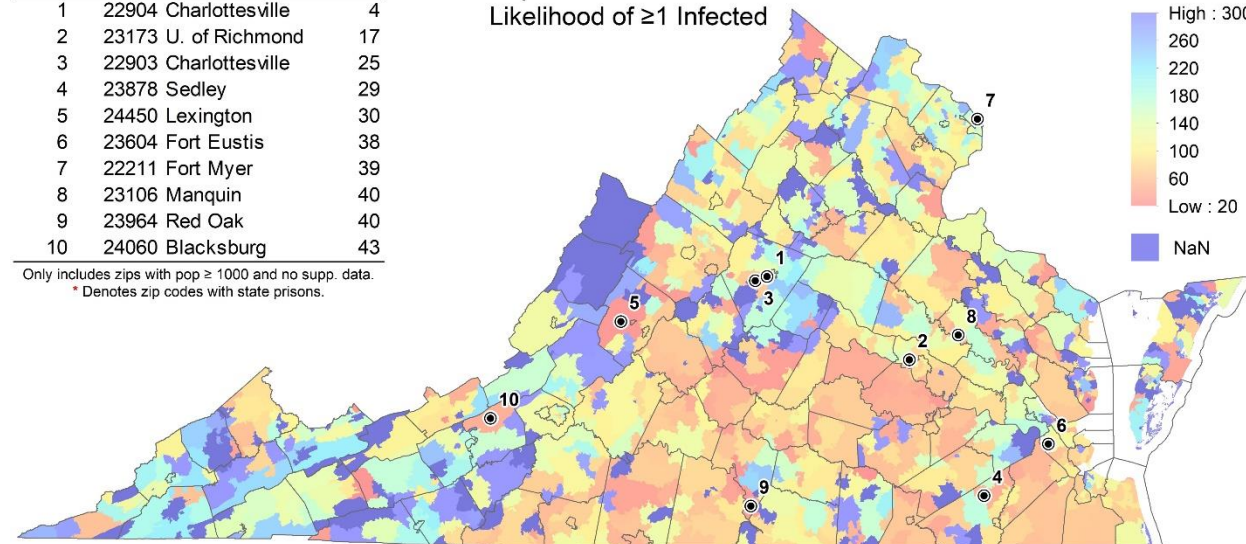
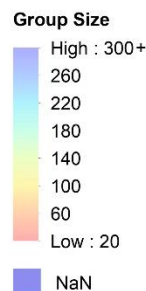
Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- Assumes 3 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey)
- On left, minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 14 in Hanover, there is a 50% chance someone will be infected)
- Some zip codes have high likelihood of exposure even in groups of 25

Rank	Zip Code	Name	Size
1	22904	Charlottesville	4
2	23173	U. of Richmond	17
3	22903	Charlottesville	25
4	23878	Sedley	29
5	24450	Lexington	30
6	23604	Fort Eustis	38
7	22211	Fort Myer	39
8	23106	Manquin	40
9	23964	Red Oak	40
10	24060	Blacksburg	43

Only includes zips with pop ≥ 1000 and no supp. data.
 * Denotes zip codes with state prisons.

Group Size Needed for 50%
Likelihood of ≥1 Infected

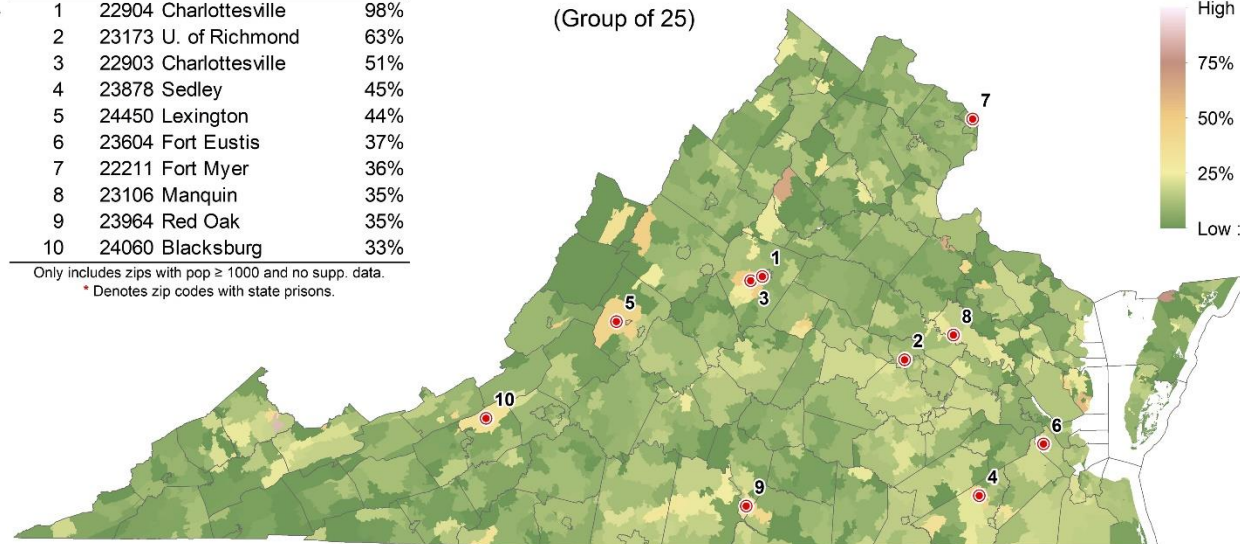
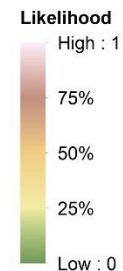


Based on zip code point prevalence for week ending 2021-02-20

Rank	Zip Code	Name	Likelihood
1	22904	Charlottesville	98%
2	23173	U. of Richmond	63%
3	22903	Charlottesville	51%
4	23878	Sedley	45%
5	24450	Lexington	44%
6	23604	Fort Eustis	37%
7	22211	Fort Myer	36%
8	23106	Manquin	35%
9	23964	Red Oak	35%
10	24060	Blacksburg	33%

Only includes zips with pop ≥ 1000 and no supp. data.
 * Denotes zip codes with state prisons.

Likelihood of ≥1 Infected Members
(Group of 25)



Based on zip code point prevalence for week ending 2021-02-20

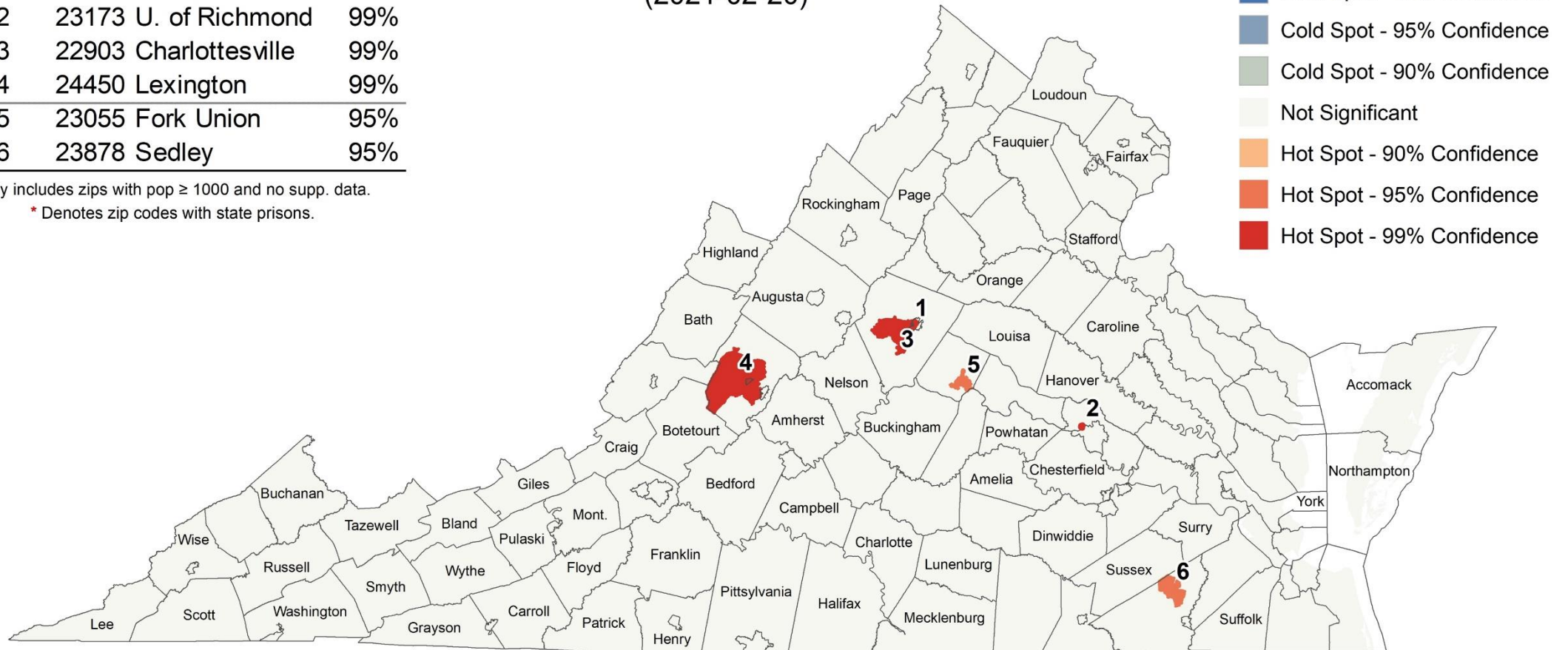
Current Spatial Hot Spots

Spot	Zip Code	Name	Conf.
1	22904	Charlottesville	99%
2	23173	U. of Richmond	99%
3	22903	Charlottesville	99%
4	24450	Lexington	99%
5	23055	Fork Union	95%
6	23878	Sedley	95%

Only includes zips with pop ≥ 1000 and no supp. data.

* Denotes zip codes with state prisons.

Point Prevalence Hot Spots by Zip Code
(2021-02-20)

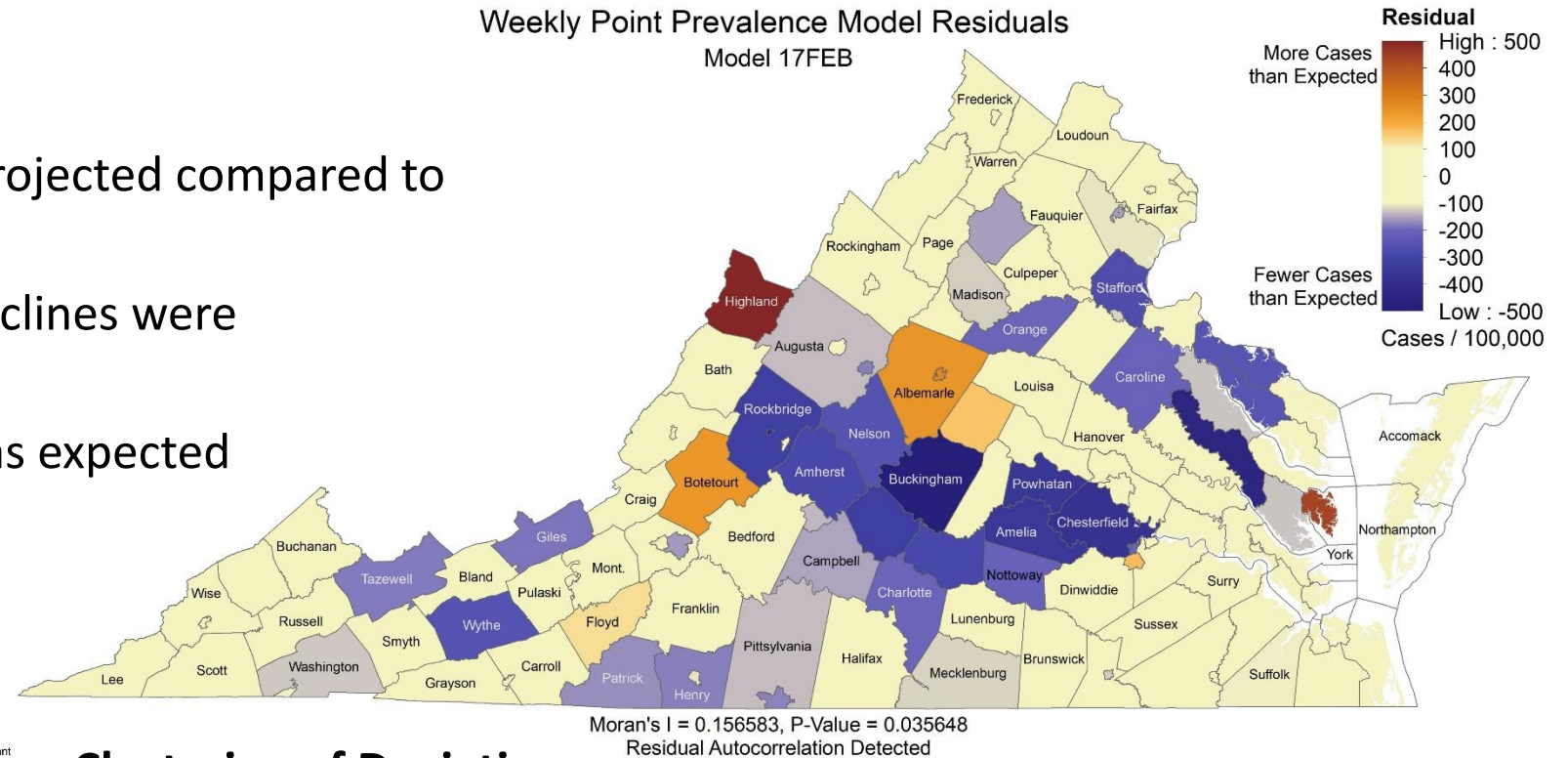


Hot Spots compare the weekly case prevalence to other zip codes in the surrounding area to identify areas with statistically significant deviations

Deviations from Model's Expectations

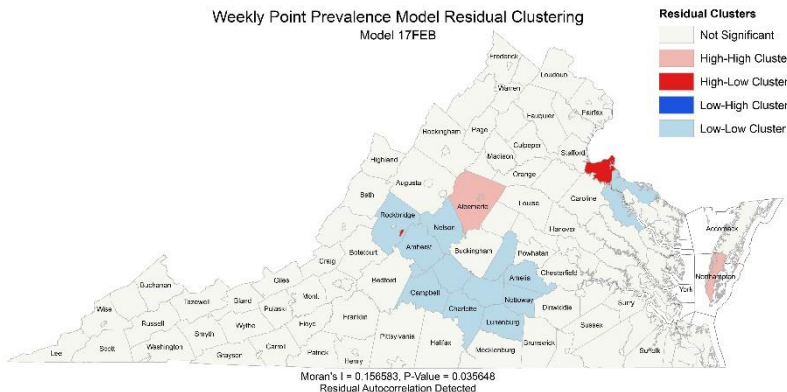
Deviations from Model's Projection

- The weekly case rate (per 100K) projected compared to observed by county
- Highlights where the growth or declines were unexpectedly strong
- Some spatial hotspots continued as expected others were significantly strong



Clustering of Deviations

- Identifies broader areas where the deviations were pronounced
- C'ville and Albemarle both more cases than expected
- Central VA fewer cases than expected



Model Update – Adaptive Fitting

Adaptive Fitting Approach

Each county fit precisely, with recent trends used for future projection

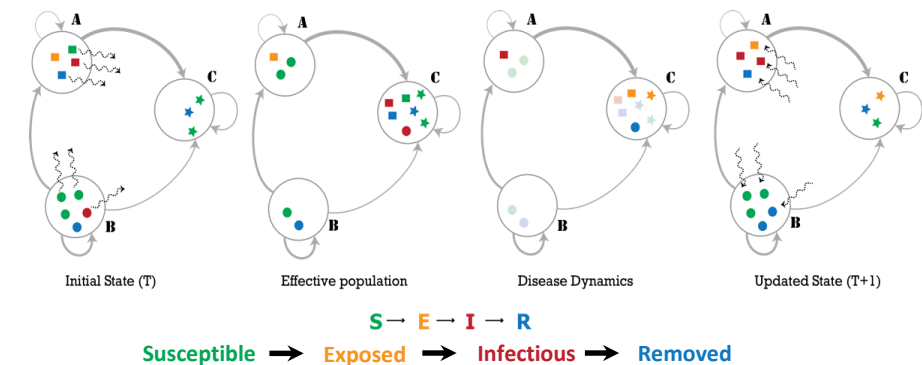
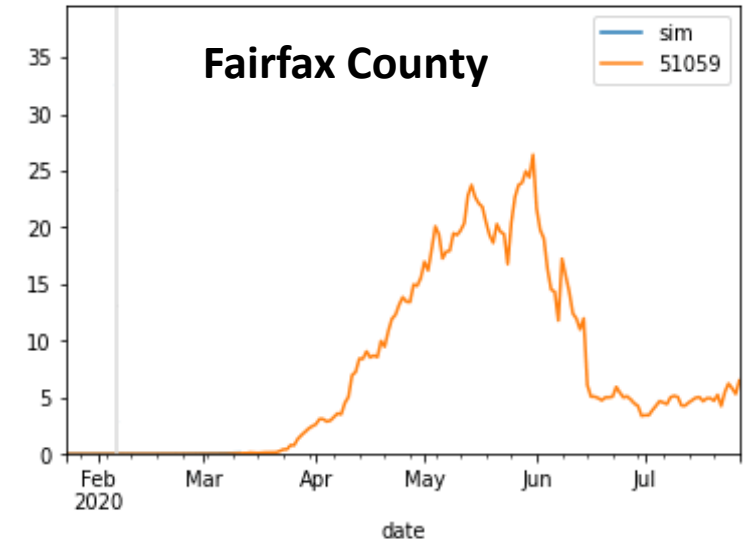
- Allows history to be precisely captured, and used to guide bounds on projections

Model: An alternative use of the same meta-population model, PatchSim

- Allows for future “what-if” Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

External Seeding: Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding



Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

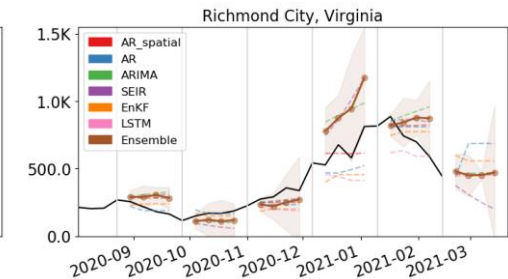
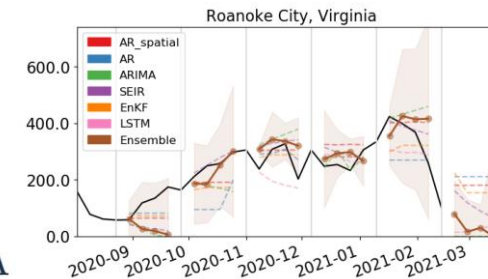
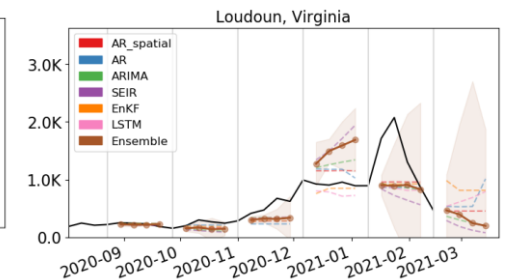
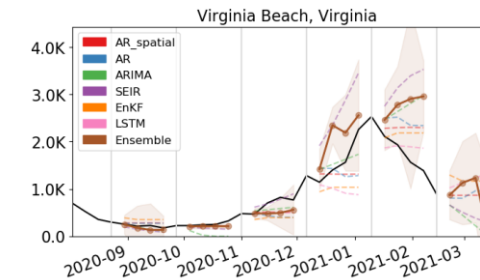
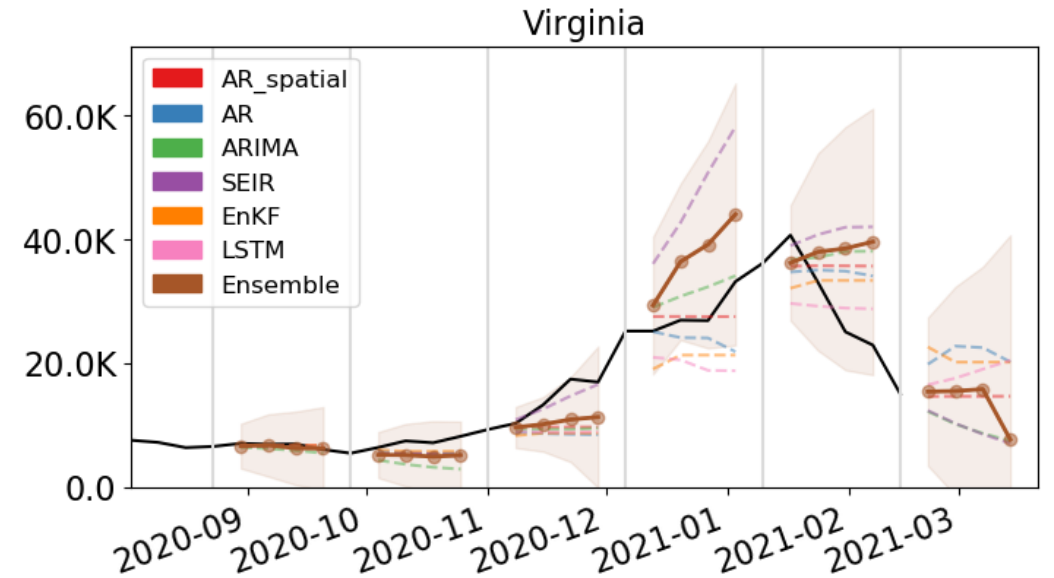
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

Weekly forecasts done at county level.

Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional 'surveillance' for making scenario-based projections.

Also submitted to CDC Forecast Hub.



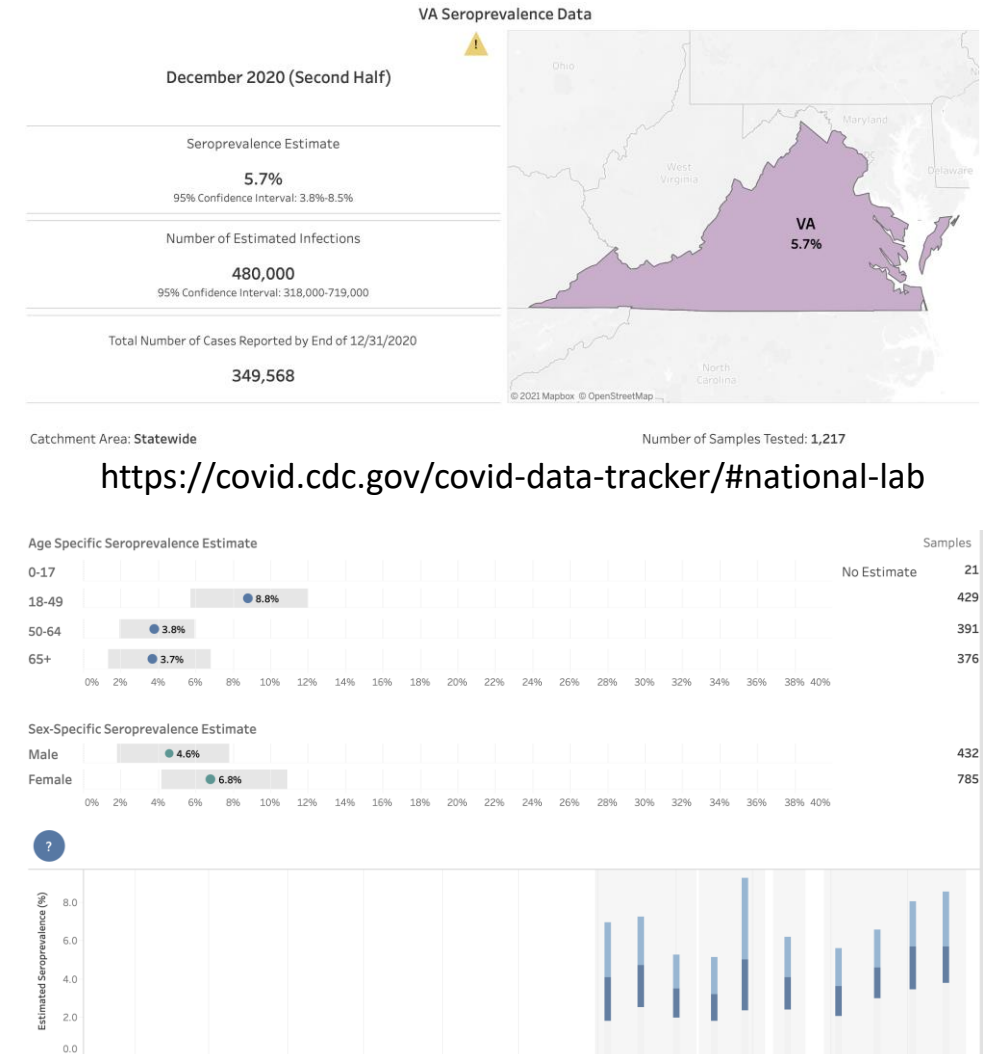
Seroprevalence updates to model design

Several seroprevalence studies provide better picture of how many actual infections have occurred

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 5.7% [3.8% – 8.5%] seroprevalence as of Dec 10th – 23rd from 4.6% a month earlier

These findings are equivalent to an ascertainment ratio of ~3x in the future, with bounds of (2x to 5x)

- Thus for 3x there are 3 total infections in the population for every confirmed case
- Uncertainty design has been shifted to these bounds (previously higher ascertainment as was consistent earlier in the pandemic were being used)



Calibration Approach

- **Data:**
 - County level case counts by date of onset (from VDH)
 - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
 - Tune transmissibility across ranges of:
 - Duration of incubation (5-9 days), infectiousness (3-7 days)
 - Undocumented case rate (1x to 7x) guided by seroprevalence studies
 - Detection delay: exposure to confirmation (4-12 days)
 - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
 - **Mean trend from last 7 days of observed cases and first week of ensemble's forecast used**
 - Outliers removed based on variances in the previous 3 weeks
 - 2 week interpolation to smooth transitions in rapidly changing trajectories

COVID-19 in Virginia:

Dashboard Updated: 2/23/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths					
Total Cases*		Total Hospitalizations**		Total Deaths	
567,039		23,698		7,658	
(New Cases: 1,769)^					
Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
447,840	119,199	22,501	1,197	6,590	1,068

* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).

** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.

^New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.

† VDH adopted the updated CDC COVID-19 confirmed and probable surveillance case definitions on August 27, 2020. Found here: <https://www.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/>

Outbreaks	
Total Outbreaks*	Outbreak Associated Cases
2,554	63,007

* At least two (2) lab confirmed cases are required to classify an outbreak.

Testing (PCR Only)	
Testing Encounters PCR Only*	Current 7-Day Positivity Rate PCR Only**
5,778,994	8.3%

* PCR* refers to "Reverse transcriptase polymerase chain reaction laboratory testing."

** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multisystem Inflammatory Syndrome in Children	
Total Cases*	Total Deaths
25	0

*Cases defined by CDC HAN case definition: <https://emergency.cdc.gov/han/2020/han00432.asp>

Accessed 8:30am February 24, 2021

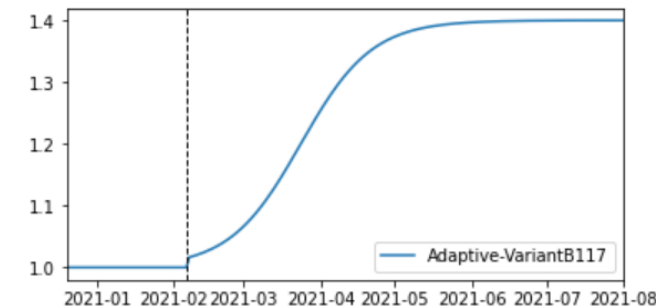
<https://www.vdh.virginia.gov/coronavirus/>

Scenarios – Seasonal Effects

- Variety of factors continue to drive transmission rates
 - Seasonal impact of weather patterns, travel and gatherings, fatigue and premature relaxation of infection control practices.
- Plausible levels of transmission can be bounded by past experience
 - Assess transmission levels at the county level since May 2020
 - Use the highest and lowest levels experienced (excluding outliers) as plausible bounds for levels of control achievable
 - Transition from current levels of projection to the new levels over 2 months
- New planning Scenarios:
 - **Best of the Past:** Lowest level of transmission (10th percentile)
 - **Fatigued Control:** Highest level of transmission (95th percentile) increased by additional 5%

Scenarios – Novel Variants

- Several novel variants of SARS-CoV2 are being tracked
 - Some are more transmissible, some may escape immunity from previous natural infection and/or vaccination, others may be more severe
- New Variant B.1.1.7 is best understood and is in Virginia
 - **Transmission increase:** [Several different studies](#) have estimated the increase in transmission to be 30-55%, we use 40% increase from the current baseline projection
 - **Emergence timing:** Gradually assumes predominance over the next 6 weeks, reaching 50% frequency in late March as estimated in a recent [MMWR report from CDC](#) and refined by [Andersen et al.](#)
- Variant planning Scenario:
 - **VariantB117:** Current projected transmissibility increases gradually over 4 months to level 40% more transmissible



Scenarios – Vaccines

- Vaccination has started, and efforts are underway to increase its pace
 - Exact achievable rollouts and level of coverage are unknown, though coming into focus
- Vaccine efficacy varies over course of vaccine
 - FDA EUAs show 50% efficacy achieved 2 weeks after 1st dose, and 95% 2 weeks after 2nd dose
 - Assuming 3.5 week (average of Pfizer and Moderna) gap between doses
- Vaccine hesitancy poses a future problem
 - Currently demand far outpaces supply so we assume all courses will be administered until we reach the hesitancy threshold, for 50% this is several months in the future.

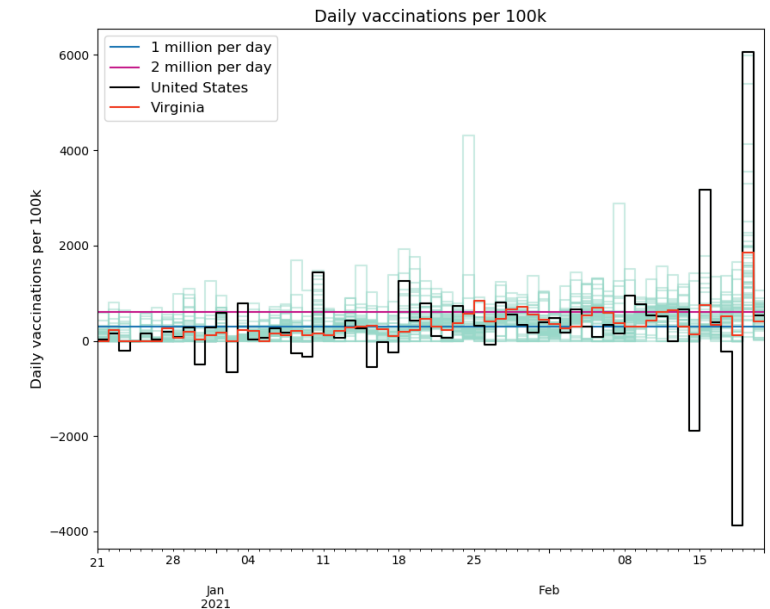
Current rollouts and scenarios inspired by
MIDAS Network COVID-19 Scenario Hub:
<https://github.com/midas-network/covid19-scenario-modeling-hub>

24-Feb-21

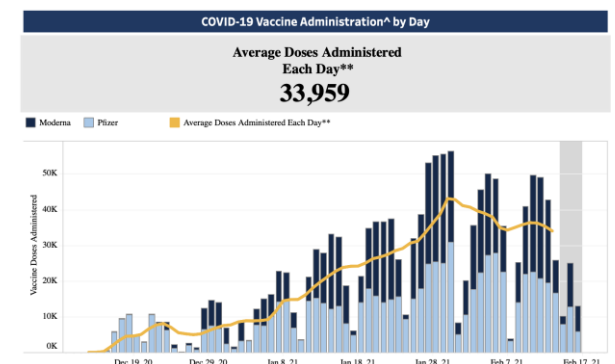


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VA Vaccination Rates



Lines represent 1M & 2M total doses administered a day (rate of 303/100K & 606/100K)



Accessed 3:30pm February 17, 2021
<https://www.vdh.virginia.gov/coronavirus/covid-19-vaccine-summary/>

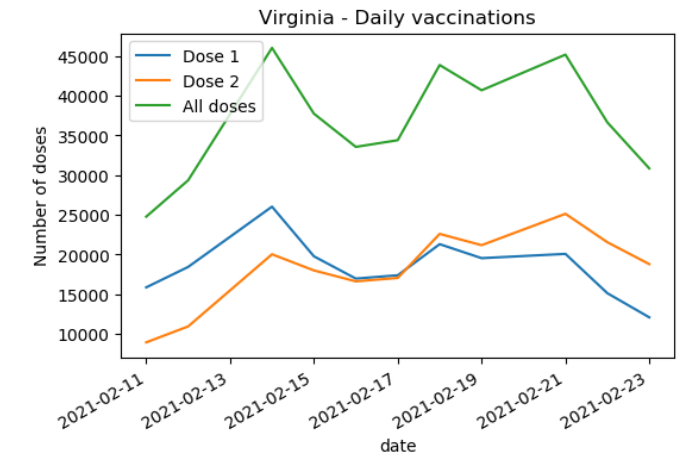
31

Scenarios – Vaccines

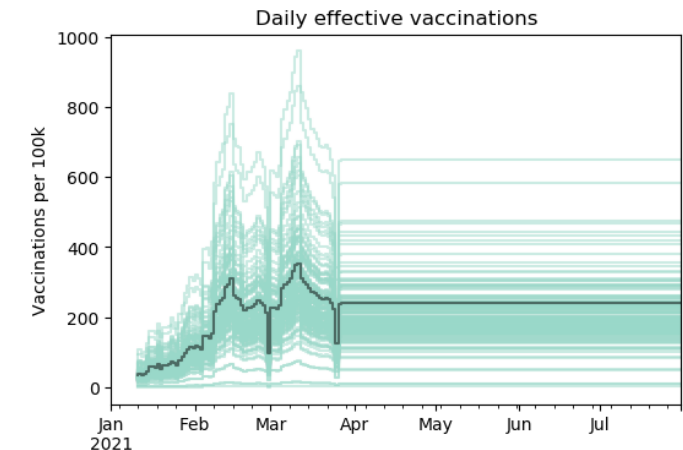
- Administration schedule uses actual administration and expected for the future
 - Use history of state-specific doses administered as captured by [Bloomberg](#) (up to Jan 19th) and [CDC](#) (Jan 20th and on)
 - Vaccination rate specific to each county (as obtained through VDH dashboard) vax data in data package
 - Future courses based on sustaining daily average of most recent week
 - Rate:** 252 **FIRST DOSES** per 100K per day or a total of ~21K 1st doses per day, which is up from last week's levels
 - Total Amount:** This pace leads to eventually reaching 42K administered a day, implying 21K fully vaccinated a day
 - Location:** Per capita distribution across all counties

Current rollouts and scenarios inspired by MIDAS Network COVID-19 Scenario Hub: <https://github.com/midas-network/covid19-scenario-modeling-hub>

Fluctuations in dosages over time



Modeled Vaccine Induced Immunity



All VA counties, median in black

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these seasonal effects and use the updated vaccine schedule

- **Adaptive:** No seasonal effects from base projection
 - If things continue as they are
- **Adaptive-FatigueControl:** Fatigued control seasonal effects
 - If we revert to slightly worst transmission experienced in last 6 months
- **Adaptive-BestPast:** Best of the past control seasonal effects
 - If we revert to best control experienced in last 6 months
- **Adaptive-VariantB117:** Boosting of transmissibility from the emergence of B.1.1.7
 - If new variants begin to predominate and boost transmission, this assumes current seasonal affects remain the same (eg like Adaptive)
- **Adaptive-FatigueControl-VariantB117:** Fatigued control and txm boost from B.1.1.7
- **Adaptive-BestPast-VariantB117:** Best of the past control vs. txm boost from B.1.1.7

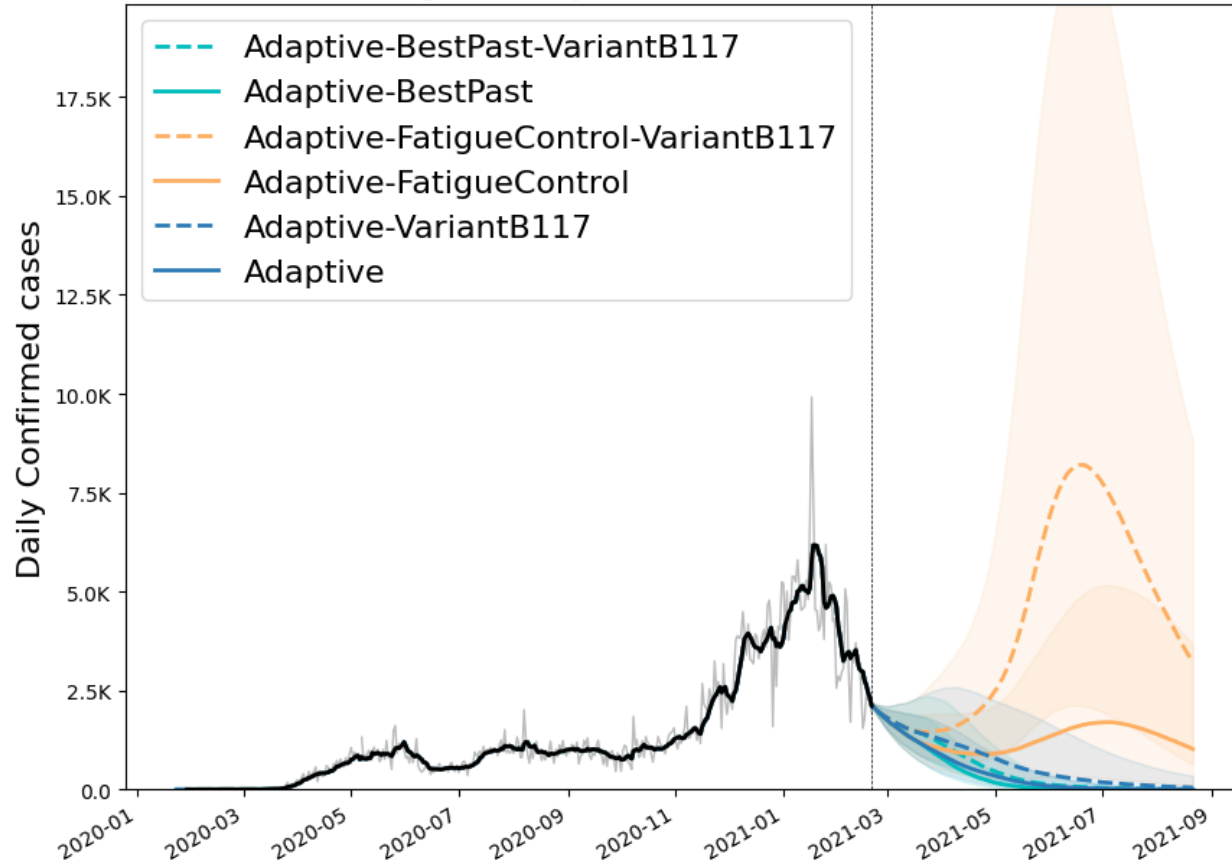
Counterfactuals with no vaccine (“NoVax”) are provided for comparison purposes

Model Results

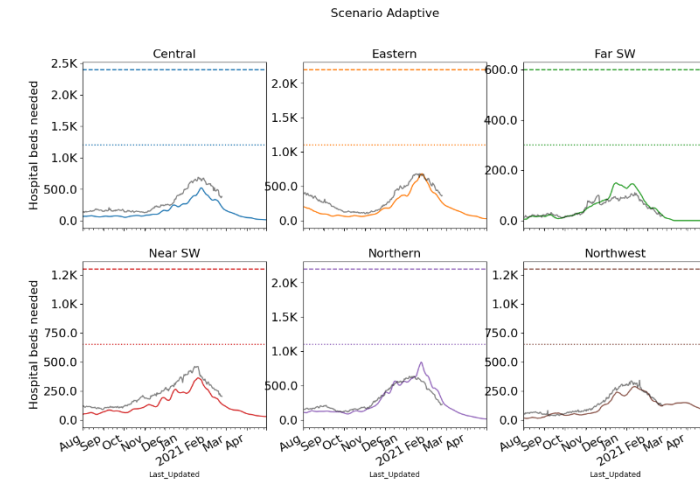
Outcome Projections

Confirmed cases

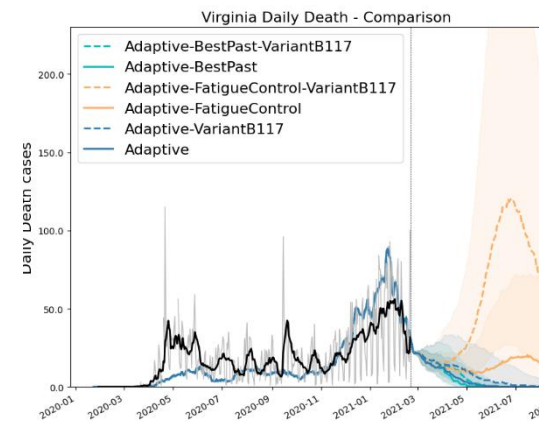
Virginia Daily Confirmed - Comparison



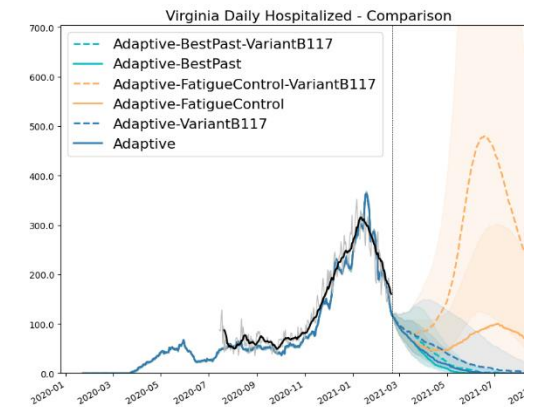
Estimated Hospital Occupancy



Daily Deaths



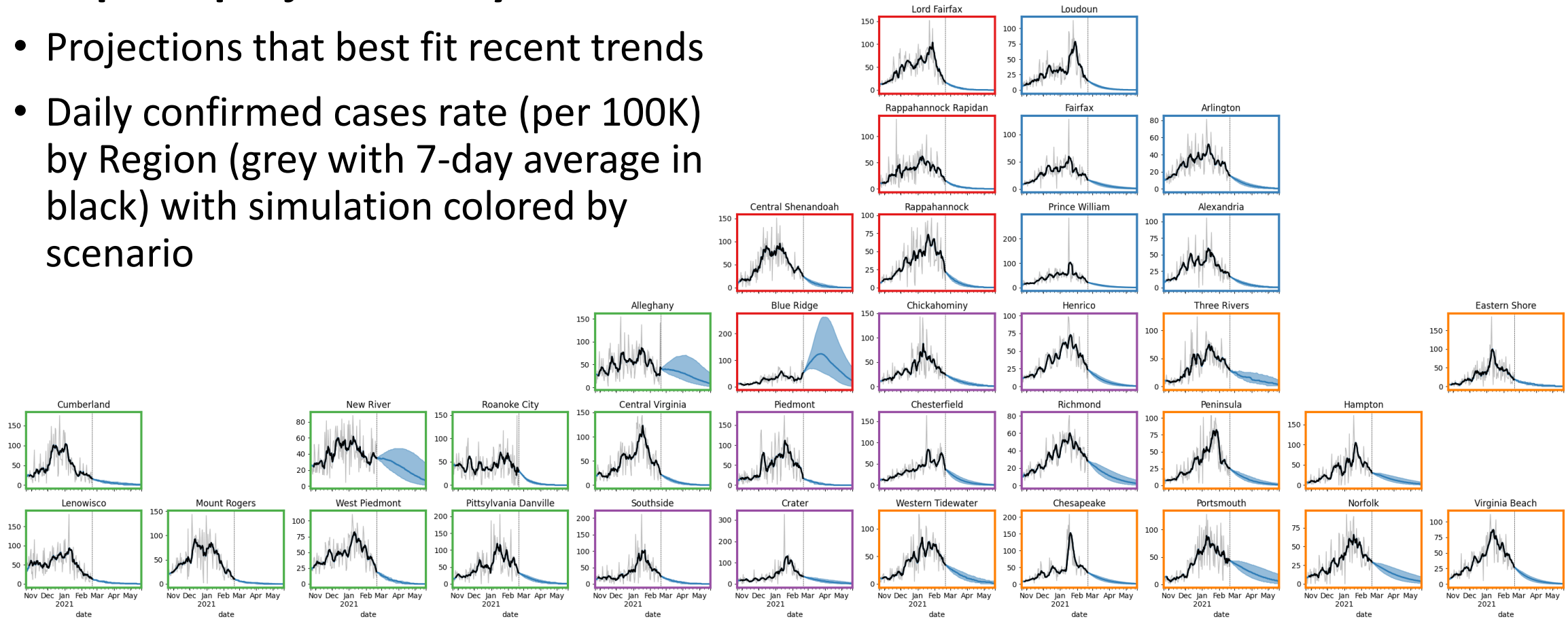
Daily Hospitalized



District Level Projections: Adaptive

Adaptive projections by District

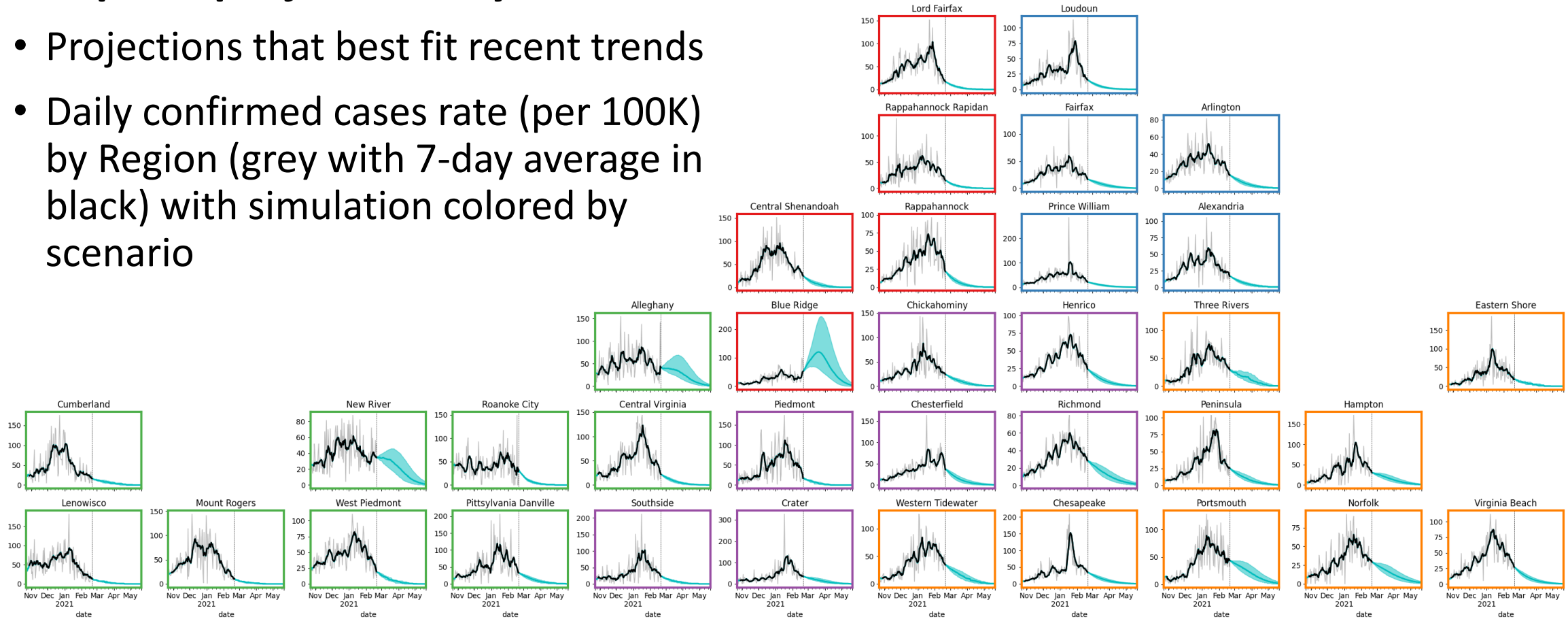
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-BestPast

Adaptive projections by District

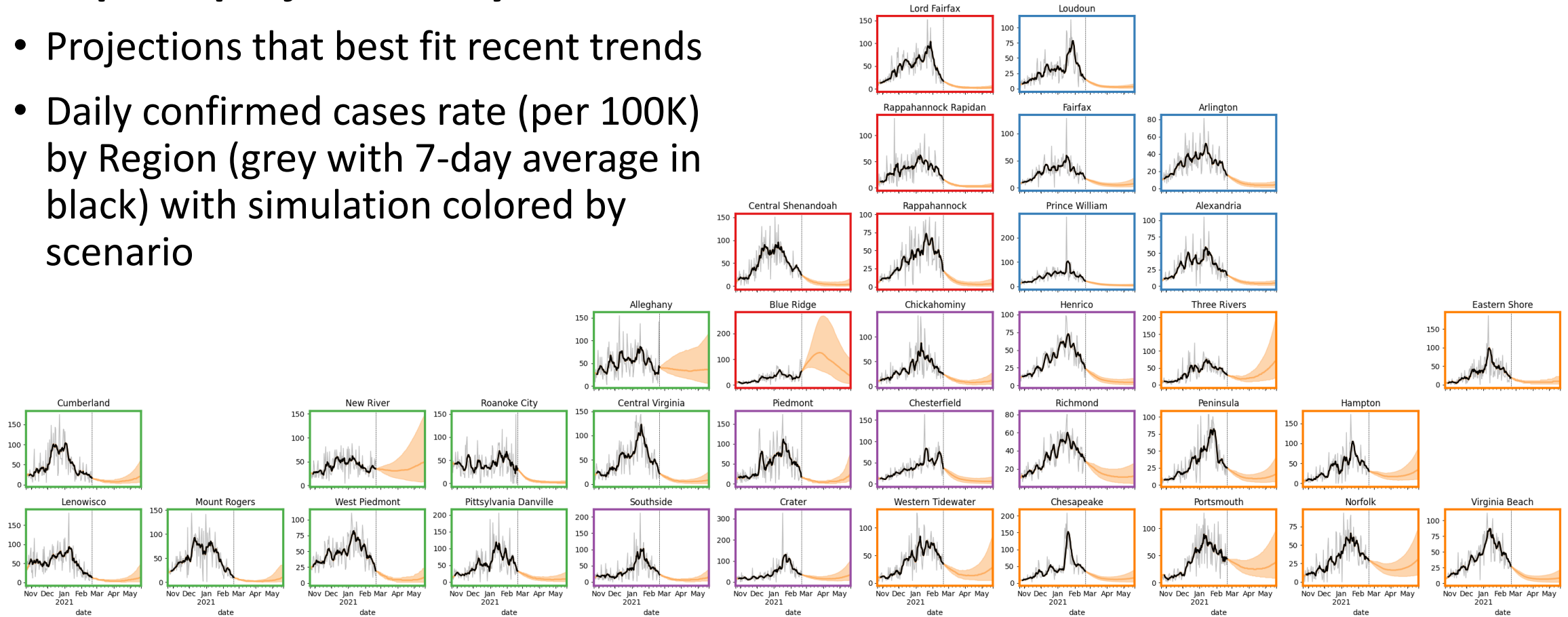
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl

Adaptive projections by District

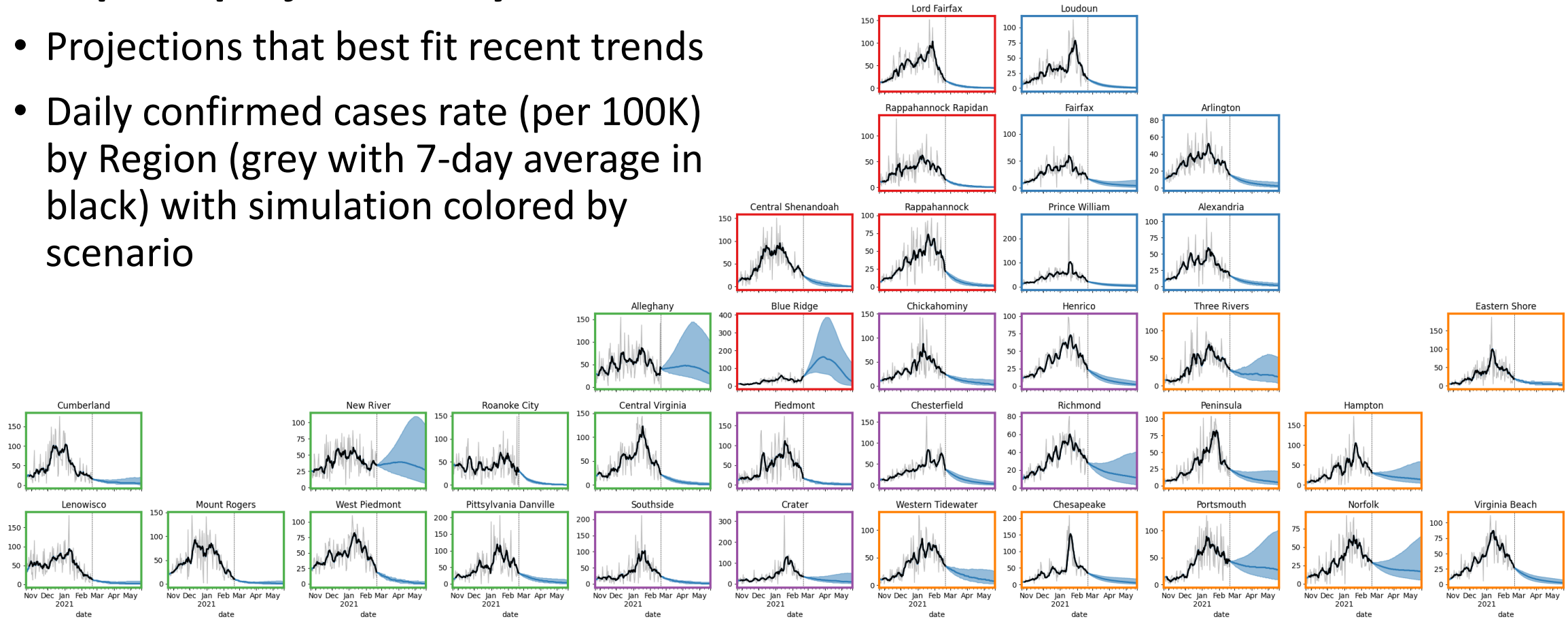
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-VariantB117

Adaptive projections by District

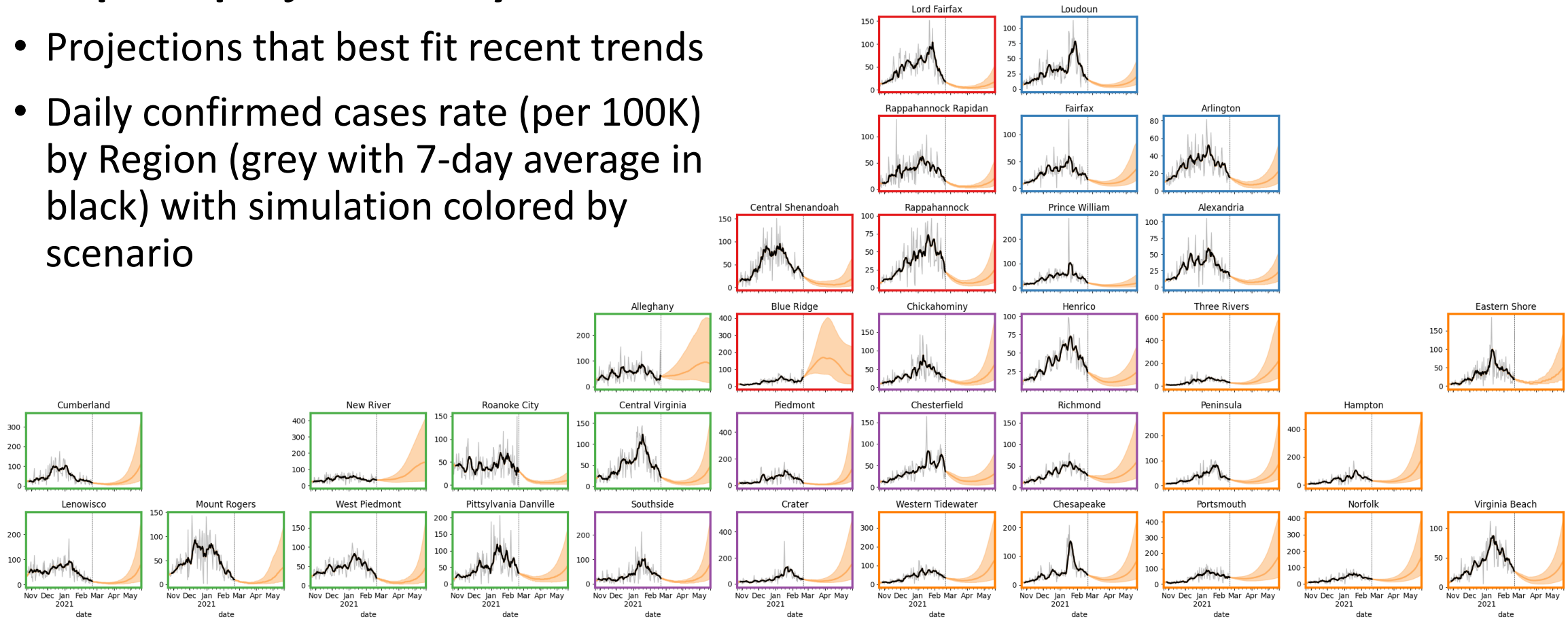
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl-VariantB117

Adaptive projections by District

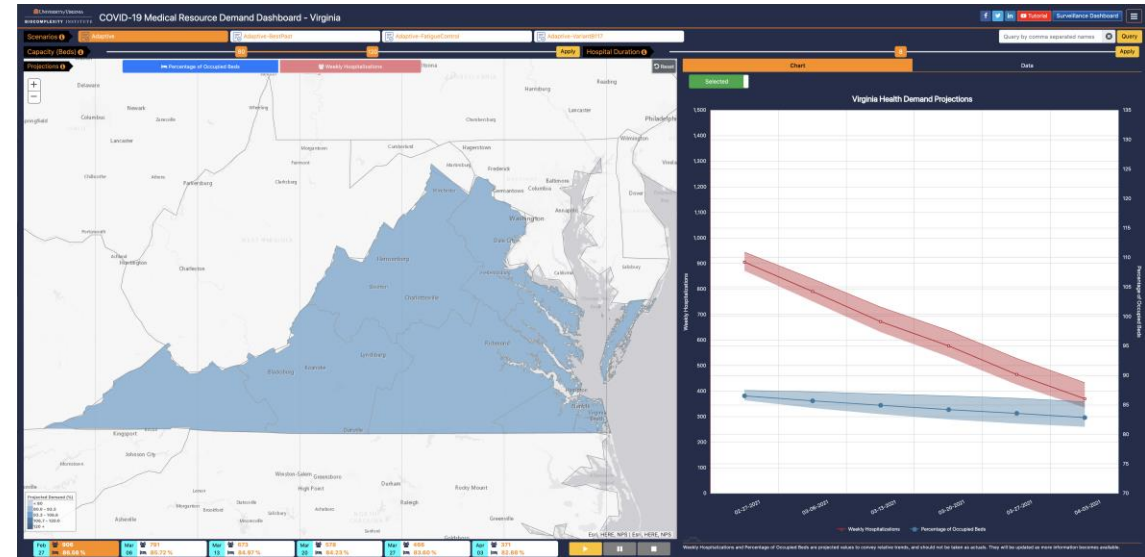
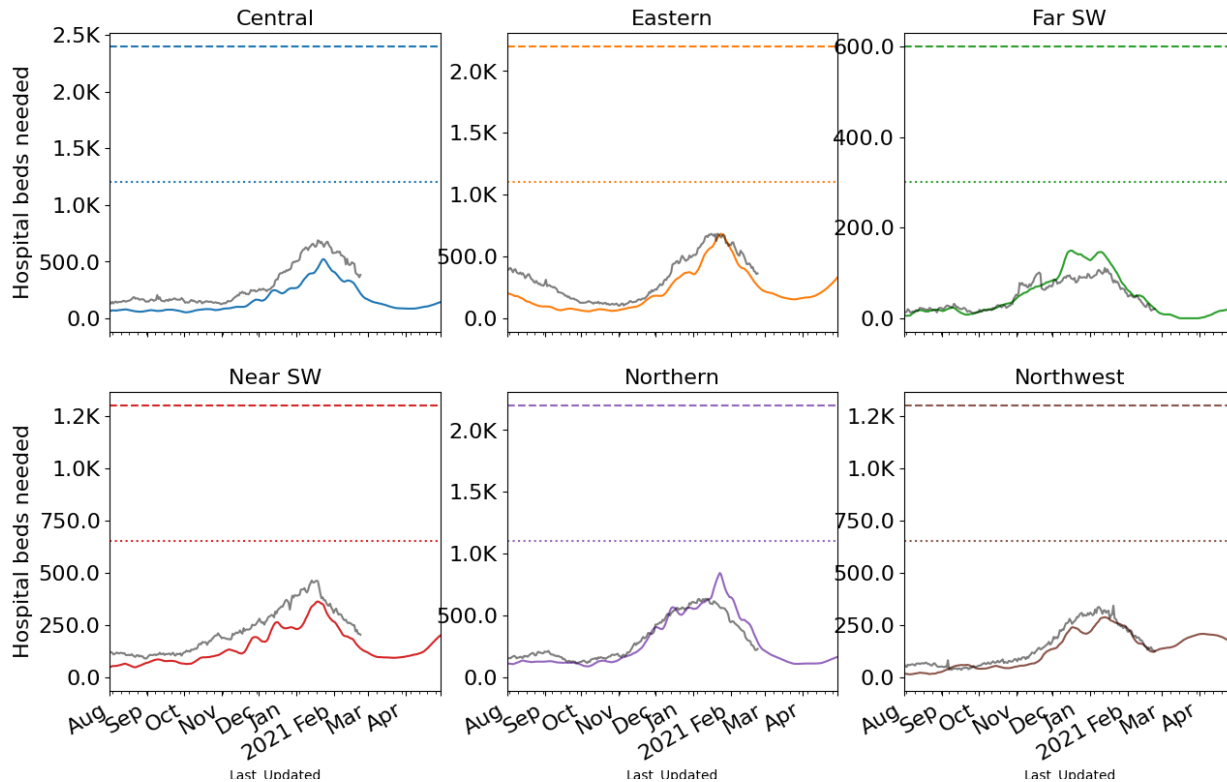
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl-VariantB117

COVID-19 capacity ranges from 80% (dots) to 120% (dash) of total beds



<https://nssac.bii.virginia.edu/covid-19/vmrddash/>

If Adaptive-FatigueControl-Variant scenario:

- Surge bed capacity is unlikely to be reached in coming 4 months

* Assumes average length of stay of 8 days
24-Feb-21

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/21/21	17,365	17,367	17,365	17,365	17,367
2/28/21	13,349	13,346	13,344	13,495	13,504
3/7/21	11,443	11,417	11,436	12,086	12,115
3/14/21	9,851	9,834	9,847	10,976	11,011
3/21/21	8,481	8,531	8,441	10,156	10,285
3/28/21	7,245	7,743	6,994	9,498	10,242
4/4/21	6,079	7,175	5,504	8,767	10,507
4/11/21	4,943	6,668	4,097	8,050	11,134
4/18/21	3,988	6,374	2,958	7,357	12,317
4/25/21	3,233	6,277	2,077	6,578	14,068
5/2/21	2,577	6,326	1,383	5,718	16,609
5/9/21	1,997	6,593	897	4,858	20,309

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/21/21	992	993	992	992	993
2/28/21	750	750	750	760	760
3/7/21	627	624	626	665	667
3/14/21	543	543	543	604	605
3/21/21	462	463	460	563	570
3/28/21	384	419	370	522	568
4/4/21	322	379	288	468	592
4/11/21	264	342	210	428	619
4/18/21	205	328	142	396	694
4/25/21	157	328	100	358	815
5/2/21	134	328	77	306	952
5/9/21	102	349	41	254	1,184

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 23/100K from 34/100K, US levels decline (to 19 from 23 per 100K)
- Significant progress made in last month, however 92% of VA counties above mean rate of Summer 2020
- Projections are down across Commonwealth, though several districts with universities are notably up
- Recent updates:
 - Variant B.1.1.7 scenarios included and added to control-based scenarios
 - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- The situation is changing rapidly. Models continue to be updated regularly.

References

Venkatramanan, S., et al. "Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints." *PLoS computational biology* 15.9 (2019): e1007111.

Arindam Fadikar, Dave Higdon, Jiangzhuo Chen, Bryan Lewis, Srinivasan Venkatramanan, and Madhav Marathe. Calibrating a stochastic, agent-based model using quantile-based emulation. *SIAM/ASA Journal on Uncertainty Quantification*, 6(4):1685–1706, 2018.

Adiga, Aniruddha, Srinivasan Venkatramanan, Akhil Peddireddy, et al. "Evaluating the impact of international airline suspensions on COVID-19 direct importation risk." *medRxiv* (2020)

NSSAC. PatchSim: Code for simulating the metapopulation SEIR model. <https://github.com/NSSAC/PatchSim> (Accessed on 04/10/2020).

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Biocomplexity Institute. COVID-19 Surveillance Dashboard. <https://nssac.bii.virginia.edu/covid-19/dashboard/>

Google. COVID-19 community mobility reports. <https://www.google.com/covid19/mobility/>

Biocomplexity page for data and other resources related to COVID-19: <https://covid19.biocomplexity.virginia.edu/>

Questions?

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Supplemental Slides

Date of Onset Reproductive Number

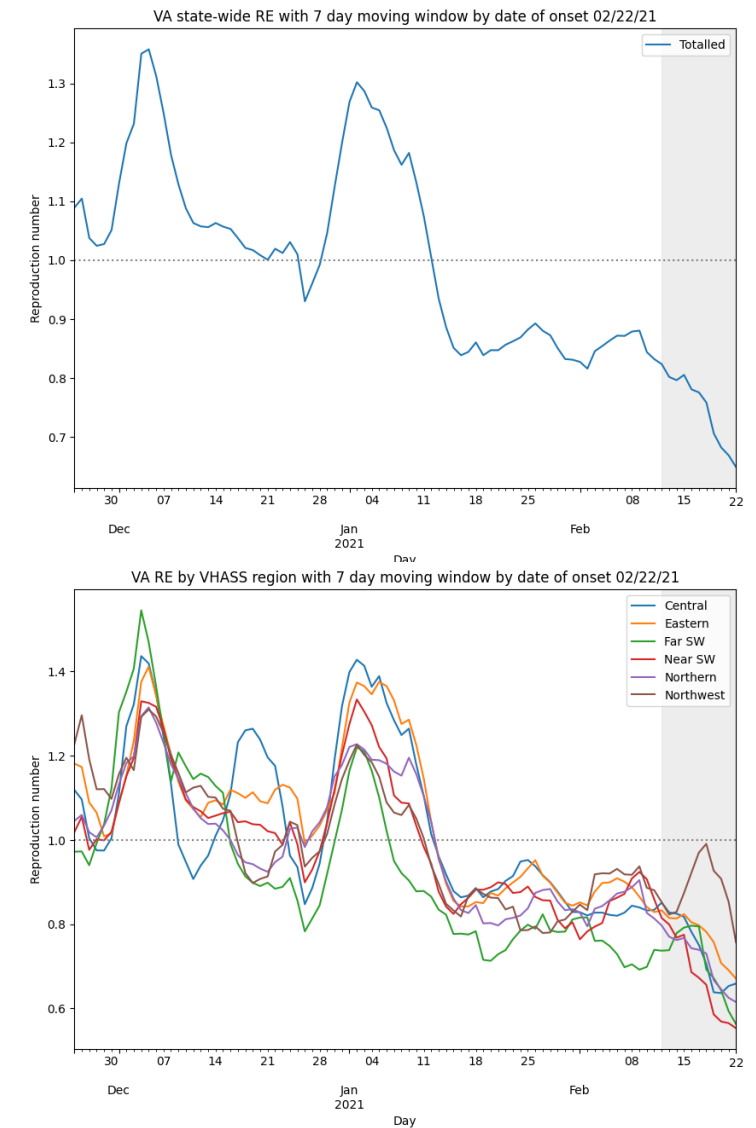
Feb 13th Estimates

Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.802	-0.042
Central	0.828	0.020
Eastern	0.815	-0.063
Far SW	0.738	0.029
Near SW	0.799	-0.037
Northern	0.770	-0.068
Northwest	0.823	-0.064

Methodology

- Wallinga-Teunis method (EpiEstim¹) for cases by date of onset
- Serial interval: 6 days (2 day std dev)
- Recent estimates may be unstable due to backfill

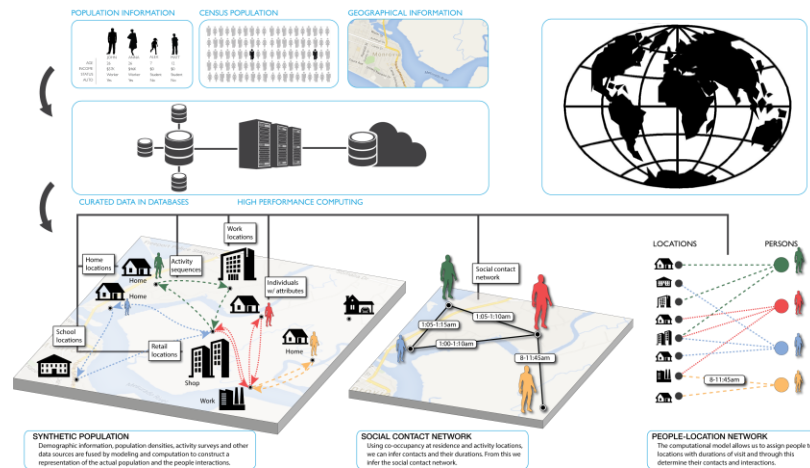
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, <https://doi.org/10.1093/aje/kwt133>



Agent-based Model (ABM)

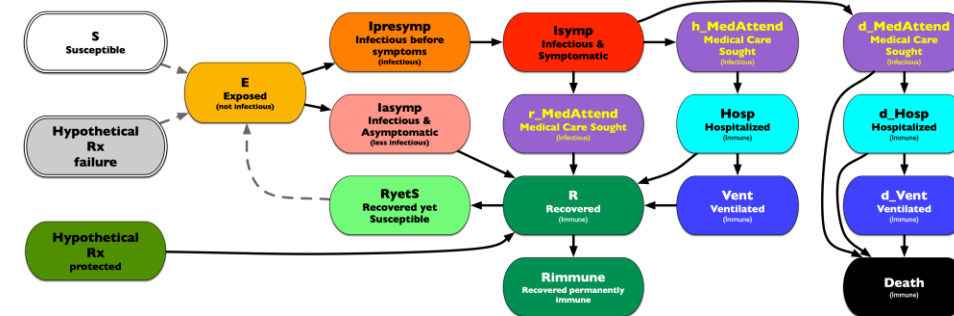
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



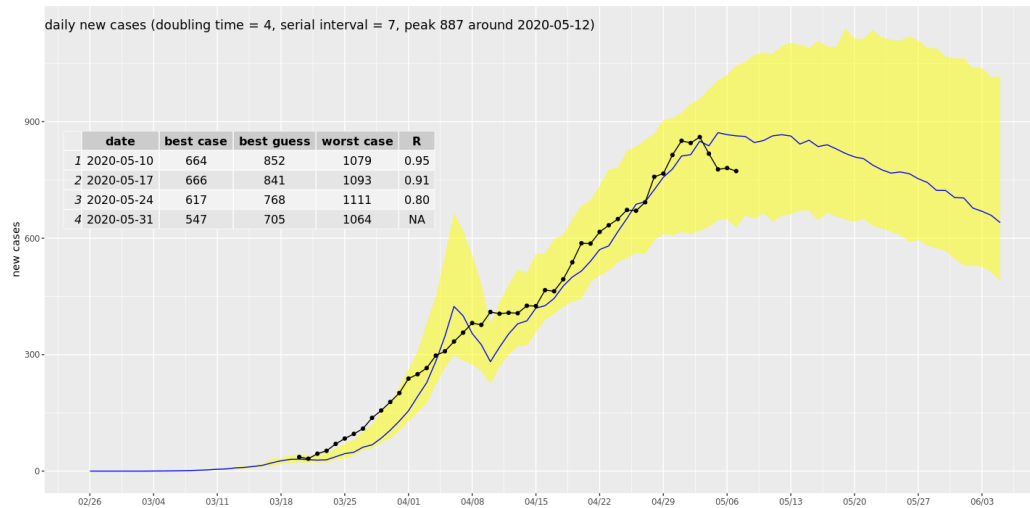
Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

ABM Social Distancing Rebound Study Design

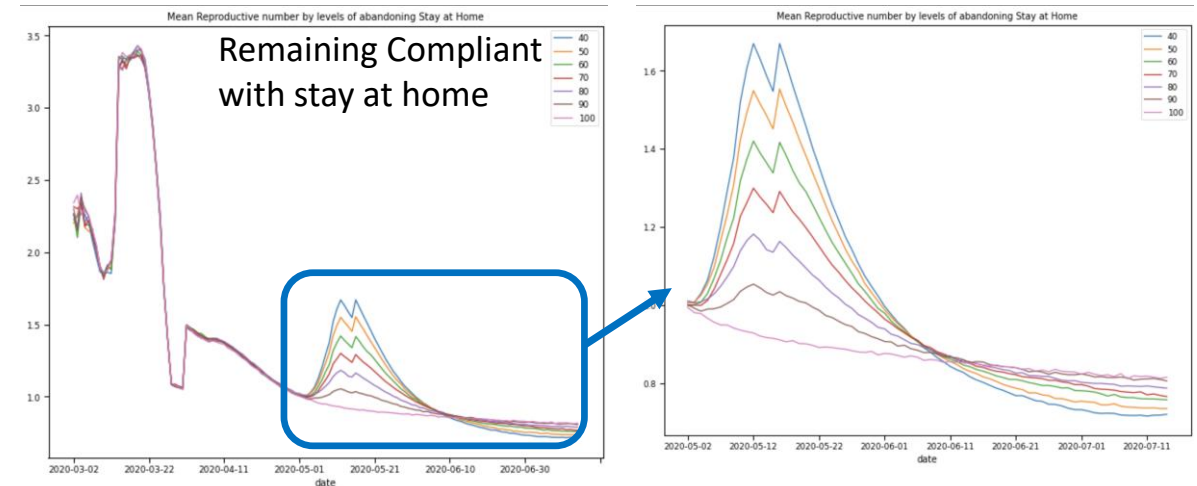
Study of "Stay Home" policy adherence

- Calibration to current state in epidemic
- Implement "release" of different proportions of people from "staying at home"



Calibration to Current State

- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim



Impacts on Reproductive number with release

- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a $1/6^{\text{th}}$ return to pre-pandemic levels